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	Document Number 1650775	Unigene Cluster Title	B-cell translocation gene 1, anti- proliferative	B-cell translocation gene 1, anti- proliferative	Rattus norvegicus sulfate anion transporter (sat-1) mRNA, complete cds	ATPase, Cu++ transporting, beta	Adrenergic, alpha 1B- recentor	Rat protein-glutamine gamma- glutamyltransferase mRNA, complete cds	Rattus norvegicus nuclear receptor Rev- FrhA-heta mRNA partial ode			Rattus norvegicus mRNA for beta-	alanine oxoglutarate aminotransferase,	complete cds			Bathis nocyenicis mBNA for boto	alanine oxodlufarate aminotransferase	complete cds
		Known Gene Name	B-cell translocation gene 1, anti- proliferative	B-cell translocation gene 1, anti- proliferative	HMm:alpha-L-iduronidase	ATPase, Cu++ transporting, beta	Adrenergic, alpha 1B-, receptor	HSp:PROTEIN-GLUTAMINE GAMMA- GLUTAMYLTRANSFERASE K						HHs:4-aminobutyrate aminotransferase complete cds					HHs:4-aminobutyrate aminotransferase complete cds
	111111111111111111111111111111111111111	Fathways			Glycosaminoglycan degradation	Oxidative phosphorylation				Alanine and aspartate	metabolism, Butanoate metabolism, Glutamate	metabolism, Propanoate	metabolism, beta-Alanine	metabolism	Alanine and aspartate	metabolism, Glutamate	metabolism, Propanoate	metabolism,beta-Alanine	metabolism
	GenBank	21224	1729 NM_017258	1729 NM_017258	1698 NM_022287	1535 NM 012511	1620 NM 016991	1420 M57263	1454 U20796				1346 087820	D0/039					1346 D87839
	Nucleotide n Sequence ID	2	1729	1729	1698	1535	1620	1420	1454				1346	1340					1346
TABLE 1	GLGC Comparison		7 S	20 L,N	43 E,P	. 55 0	64 H	72 F	90 E				134 A				-	L	135/A

TOTAL CONTRACT

Document Number 1650775	Unigene Cluster Title	Rattus norvegicus ebnerin mRNA, complete cds	Rattus norvegicus ebnerin mRNA, complete cds	Rat mRNA for mitochondrial malate	Rattus norvegicus complement C8 beta (C8b) mRNA, partial cds	Cystathionine beta synthase	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds	Rattus norvegicus AKAP95 mRNA, partial cds	Rattus norvegicus GADD45 mRNA, complete cds	Rattus norvegicus GADD45 mRNA, complete cds	Rattus norvegicus GADD45 mRNA, complete cds	Rattus norvegicus GADD45 mRNA, complete cds
	Known Gene Name	crp-ductin	crp-ductin	Malate dehydrogenase 2, NAD (mitochondrial)		Cystathionine beta synthase			HHs:growth arrest and DNA-damage-inducible, alpha			
	Pathways			Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism		Glycine, serine and threonine metabolism, Methionine metabolism, Selenoamino acid metabolism						
	GenBank Acc ID	1712 NM_022849	1712 NM_022849	538 AI010480	1452 U20194	1538 NM_012522	1251 Al235460	1443 U01914	1720 NM_024127	1720 NM 024127	1720 NM_024127	1720 NM_024127
	Nucleotide Sequence ID	1712	1712	538	1452	1538	1251	1443	1720 1	1720 [1720 1	1720
E 1	GLGC Comparison	154 P,Q	۵	工	D	0	~	D	А	A,J	353 A,B,C,J	354 A,J,Q
TABLE	01 2979	154	155 P	164	228 D	291	330 R	347	351	352 A,J	353	354

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Document Number 1650775	Unigene Gluster Title		CAMP responsive element modulator	CAMP responsive element modulator	RNA editing deaminase of glutamate receptors	Rattus norvegicus prostaglandin E	receptor EP2 subtype mRNA, complete	cds	Canalicular multispecific organic anion	transporter	Rattus norvegicus alternatively spliced	signal transducer and regulator of	transcription 5a2 (STAT5a2) mRNA,	partial cds	Rattus norvegicus brain cytosolic acyl	coenzyme A thioester hydrolase mRNA,	complete cas	Rattus norvegicus brain cytosolic acyl	coenzyme A thioester hydrolase mRNA,	complete cds,acyl-CoA hydrolase	Rat tryptophan-2,3-dioxygenase mRNA,	complete cds	R.norvegicus mRNA for pl 5.5 esterase (ES-3)
	Known Gene Name	CAMP responsive element modulator, transcriptional repressor			RNA editing deaminase of glutamate receptors				multispecific organic anion	transporter						ENZYME A	I TIOES I EN TIUNOLASE			acyl-CoA hydrolase		-	Hsp.LIVER CARBOXYLESTERASE 3 F
	Pathways.																	-				Fryptophan metabolism	
	GenBank Acc ID		1600 NM_013086	1658 NM_017334	1728 NM_012894		1	1482 U94708		1578 NM_012833				1457 U25137		1464 1140604	043034			1614 NM_013214		1734 NM_022403	1517 X81395
	Nucleotide Sequence ID		1600	1658	1728			1482		1578				1457		1464	101			1614		1734	1517
TABLE1	GLGC Comparison 1D Code		355 N	356 N	360 R			372 F,M	1	373 P				384 0		30E	IAI OGO			397 S		402 N	466 L

7.5	Nucleotide				Document Number 1650775
Se	Sequence ID	GenBank Acc ID	n Pathways	Known Gene Name	
					ESTs, Moderately similar to
	1224	1004 01033808			LYSOSOMAL ALPHA-MANNOSIDASE
				Cytochrome P450, subfamily I	Cytochrome P450, subfamily I (aromatic
			Fatty acid metabolism,	(aromatic compound-inducible),	compound-inducible), member A1 (C6,
	1350	1350 E00717	Tryptophan metabolism	member A1 (C6, form c)	form c)
				Cytochrome P450, subfamily I	Cytochrome P450, subfamily I (aromatic
			Fatty acid metabolism,	(aromatic compound-inducible),	compound-inducible), member A1 (C6,
	1540	1540 NM_012540	Tryptophan metabolism	member A1 (C6, form c)	form c)
1	1581	1581 NM_012880		Superoxide dimutase 3	Superoxide dimutase 3
	405	402 AA956278			ESTs
	1575	575 NM_012803		Protein C	Protein C
				Complement component 4 binding	Complement component 4 binding
	1536	1536 NM_012516		protein, alpha	protein, alpha
					R.norvegicus mRNA for (S)-2-hydroxy
-	1169	1169 AI232087			acid oxidase
					R.norvegicus mRNA for (S)-2-hydroxy
					acid oxidase, Rattus norvegicus clone
					BB.1.4.1 unknown Glu-Pro dipeptide
	·				repeat protein mRNA, complete
	1682	1682 NM_019905		calpactin I heavy chain	cds,calpactin I heavy chain
	1146	1146 AI231127			ESTs
ł				Hsp:GLUTATHIONE S-	Rat liver glutathione S-transferase Yc
	1381	1381 K01932	Glutathione metabolism	TRANSFERASE YC-1	subunit mRNA, complete cds
į .					Rat liver glutathione S-transferase Yc
	1515	1515 X78848			subunit mRNA, complete cds
	1		-	-methylglutaryl-Coenzyme	3-hydroxy-3-methylglutaryl-Coenzyme A
	1607	1607 NM_013134	Sterol biosynthesis	A reductase	reductase

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Document Number 1650775	er Title	ıryl-Coenzyme A	jue-Dawley	ed receptor	cds	ptor	mitochondrial	on mRNA,		4 transporter	spo :	A for cytochrome	urenine	ete cds	eron inducible	A, complete cds			rimidinase,		PYS_RAT	SE	IA for	mplete cds
Document N	Unigene Cluster Title	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Rattus norvegicus Sprague-Dawley	putative G-protein coupled receptor	(GCR) mRNA, complete cds	Rat mRNA for LDL-receptor	Superoxide dimutase 2, mitochondrial	Rattus norvegicus RASP1 mRNA,	complete cds	Rattus norvegicus GABA transporter	GAT-2 mRNA, complete cds	Rattus norvegicus mRNA for cytochrome b5	Rattus norvegicus L-kynurenine	hydrolase mRNA, complete cds	Rattus norvegicus interferon inducible	protein 10 (IP-10) mRNA, complete cds			Rat mRNA for dihydropyrimidinase,	complete cds	EST, Highly similar to DPYS_RAT	DIHYDROPYRIMIDINASE	[R.norvegicus], Rat mRNA for	dihydropyrimidinase, complete cds
	Known Gene Name	3-hydroxy-3-methylglutaryl-Coenzyme 3- A reductase		<u>10.</u>)))	Low density lipoprotein receptor	Superoxide dimutase 2, mitochondrial S	<u> </u>	מכ	<u> </u>	9	<u> </u>	eninase (L-kynurenine	hydrolase) h	<u>~</u>	īd			<u>~</u>	HHs:dihydropyrimidinase c	Ш	<u>a</u>	<u> </u>	HHs:dihydropyrimidinase di
2	Pathways	Sterol biosynthesis												Tryptophan metabolism			Pantothenate and CoA	biosynthesis, Pyrimidine	metabolism,beta-Alanine	metabolism	Pantothenate and CoA	biosynthesis, Pyrimidine	metabolism,beta-Alanine	metabolism
	GenBank Acc ID	1607 NM 013134			1445 U04808	1492 X13722	1627 NM_017051		1465 U55765		1429 M95762	41 AA817685		1472 U68168		U17035				1342 D63704				1342 D63704
	Nucleotide Sequence ID	1607			1445	1492	1627		1465		1429	41		1472		1451				1342				1342
	Comparison Code	7			В	0	Ь		699 M,P		0	ď	(L	794 A,D,E,G		ſ				А				۷
TABLE	D Derec	651			671 B	672 0	682 P		669		729 0	761		794		808				811				812 A

Document Number 1650775		Unigene Cluster Title		Aldolase B, fructose-biphosphate	Rattus norvegicus laminin-5 alpha 3	Rattus norvegicus fatty acid amide	hydrolase mRNA, complete cds	Rattus norvegicus INS-1 winged helix	mRNA, complete cds	Bcl2-associated X protein	Tumor-associated glycoprotein pE4	Rattus norvegicus mRNA for PS-PLA1,	complete cds	Rattus norvegicus PSD-95/SAP90-	associated protein-2 mRNA, complete	S	Lectin, galactose binding, soluble 9	(Galectin-9)	Glutathione S-transferase 1 (theta)	Cytochrom P450 (cholesterol	hydroxylase 7 alpha)		R.norvegicus mtp1 mRNA	Cytochrome P450, subfamily IIF,	polypeptide 1	Rattus norvegicus neuron-specific enolase (NSE) mRNA, complete cds
		Known Gene Name		Aldolase B, fructose-biphosphate Ald	Ra	Ra	fatty acid amide hydrolase hyd	Ra	lmF	Bcl2-associated X protein Bc	Tumor-associated glycoprotein pE4 Tu	Ra	100	Ra	988	cds	ctose binding, soluble 9	(Galectin-9)	Glutathione S-transferase 1 (theta) Glu	olesterol	hydroxylase 7 alpha) hyd	ATP binding	cassette) R.r	Cytochrome P450, subfamily IIF, Cy	polypeptide 1 pol	Ra
		Pathways	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis,Pentose	phosphate cycle															Glutathione metabolism		Bile acid biosynthesis					
	GenBank	Acc ID		238 AA892395	381 44946108		1721 NM_024132		1480 U83112	1467 U59184	1632 NM_017076		1349 D88666			1471 U67138		1591 NM_012977	1573 NM_012796		1589 NM_012942		1500 X57523		1678 NM_019303	586 AI029917
	Nucleotide Sequence	ID.		238	381		1721		1480	1467	1632		1349			1471		1591	1573		1589		1500		1678	286
-	GLGC Comparison	Code		Ш	٥		∢		X	А	A,J		<u>a</u>			Σ		oʻ.	A		A		_		A	Z
TABLE	2979	D		820	825 4		851 A		906 K	912	923 A,J		945 P			955 M		958 I,Q	961 A		1007 A		1037		1099 A	1114 N

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GLGC Comparison		THE RESIDENCE AND ADDRESS OF THE PARTY OF TH	(1) The second of the second s			
} =		Nucleotide Segmence	GenRank	t *		
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						Rattus norvegicus cca1 mRNA,
1126 A,I		1143	1143 AI231007			complete cds
1141 E,Q	O,	1505	1505 X59601			Rat mRNA for plectin
						Rattus norvegicus NF-E2-related factor
1169 E	E,H	1008	1008 AI177161			2 mRNA, complete cds
				Fatty acid metabolism,	Cytochrome P450, subfamily IIC	Cytochrome P450, subfamily IIC
1173 A		1661	1661 NM_019184	Tryptophan metabolism	(mephenytoin 4-hydroxylase)	(mephenytoin 4-hydroxylase)
				Fatty acid metabolism,	Cytochrome P450, subfamily IIC	Cytochrome P450, subfamily IIC
1174 N		1661	1661 NM_019184	Tryptophan metabolism	(mephenytoin 4-hydroxylase)	(mephenytoin 4-hydroxylase)
				Fatty acid metabolism,	Cytochrome P450, subfamily IIC	Cytochrome P450, subfamily IIC
1175 A,E,M	,E,M	1661	NM_019184	Tryptophan metabolism	(mephenytoin 4-hydroxylase)	(mephenytoin 4-hydroxylase)
						Rattus norvegicus MAP-kinase
					HSp:DUAL SPECIFICITY PROTEIN	phosphatase (cpg21) mRNA, complete
1183		485	485 AF013144		PHOSPHATASE 5	spo
						Rattus norvegicus mRNA for gro,
1221 B	B,F,Q	1326	1326 D11445			complete cds
						Rat cystatin S (CysS) gene, complete
1223 E	111	1423	1423 M75281			cds
					Guanylate cyclase, soluble, beta 2	Guanylate cyclase, soluble, beta 2 (GTP
1246 A		1569	1569 NM_012770	Purine metabolism	(GTP pyrophosphate - lyase)	pyrophosphate - lyase)
1258		1611	1611 NM_013185		Hemopoietic cell tyrosine kinase	Hemopoietic cell tyrosine kinase
						Rat clathrin-associated adaptor protein
1271 G	ø	1384	1384 L07073			homolog (p47A) mRNA, complete cds
						Rattus norvegicus zonula occludens 2
1279 F	,,,	1477	1477 U75916			protein (ZO-2) mRNA, partial cds
1305 J		1636	1636 NM_017127	Glycerolipid metabolism	choline kinase	choline kinase
1306 J		1636	1636 NM_017127	Glycerolipid metabolism	choline kinase	choline kinase
						Rattus norvegicus GTP-binding protein
1394 G		1461	1461 U37099			(rab 3C) mKNA, complete cds

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Document Number 1650775		Unigene Cluster Title	Glucose-6-phosphate dehydrogenase	Rattus norvegicus round spermatid protein RSP29 gene, complete cds	ESTs	R.norvegicus mRNA for protein synthesis initiation factor eIF-2B delta	subunit		Dopa decarboxylase (aromatic L-amino Dopa decarboxylase (aromatic L-amino	acid decarboxylase)	proteasome (prosome, macropain)	Koratin 8	Neralli o	Rattus norvegicus S100A1 gene,Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds			Pyruvate carboxylase		Pyruvate carboxylase	Rattus norvegicus cytokeratin-18 mRNA,	partial cds
		Known Gene Name	Glucose-6-phosphate dehydrogenase	Rattus norvegicus round spermatid HHs:hydroxyacyl glutathione hydrolase protein RSP29 gene, complete cds					Dopa decarboxylase (aromatic L-amino	acid decarboxylase)	proteasome (prosome, macropain)	Subdinit, aiplia type 4	Keratin 8	Heat shock protein 70-1,S100 calcium binding protein A1			Pyruvate carboxylase		Pyruvate carboxylase		
		Pathways	Glutathione metabolism, Pentose phosphate cycle	Pvruvate metabolism				Histidine metabolism, Phenylalanine metabolism,	Tryptophan metabolism,	Tyrosine metabolism					Alanine and aspartate metabolism, Citrate cycle	(TCA cycle), Pyruvate	metabolism	Alanine and aspartate metabolism, Citrate cycle	metabolism		
	GenBank	AccID	1623 NM 017006	560 AI012802	920 AI172075		1528 Z48225			1542 NM_012545	46E1 NM 017284	107/10 1/201	1439 576054	1386 L16764			1566 NM_012744		1566 NM 012744		690 AI072634
	Nucleotide Sequence	2000	1623	560	920		1528			1542	1977 1971	1001	1439	1386			1566		1566		069
-	GLGC Comparison	Code	1399 C, D, G		C,D					Σ	L	_ [C,D				⋖		1479 A.G.K		1501 A,C,F,H
TABLE	2019 010	0	1399	1409 A	1411		1426 Q			1430 M	1447	1 100	1460 C,D	1475			1478		1479		1501

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Document Number 1650775	32	Unigene Cluster Title	ESTs	organic cationic transporter-like 1	Tropomycin 4	interleukin 18	Tumor necrosis factor receptor	Ryudocan/syndecan 2	bile acid-Coenzyme A dehydrogenase:	amino acid n-acyltransferase	Rat kidney Zn-peptidase aminopeptidase	N mRNA, complete cds	kynurenine aminotransferase II	Glycine methyltransferase		Sialophorin (gpL115, leukosianin, CD43)	Complement component 4 binding	Raftus norvenicus kallistatin mBNA	complete cds	Rattus norvegicus Sprague/Dawley	PHAS-I mRNA, complete cds	Rattus norvegicus Sprague/Dawley	PHAS-I mRNA, complete cds	Rat small nuclear ribonucleoparticle-	associated protein (snRNP) mRNA,	complete cds, clone Sm51
		Known Gene Name		organic cationic transporter-like 1	Tropomycin 4	interleukin 18	Tumor necrosis factor receptor	Ryudocan/syndecan 2	bile acid-Coenzyme A dehydrogenase:	amino acid n-acyltransferase		Leucine arylaminopeptidase 1	kynurenine aminotransferase II	Glycine methyltransferase	Sialophorin (gpL115, leukosianin,	CD43)	Complement component 4 binding	protein, bota								
	i i i ce kango:	Pathways							Bile acid biosynthesis, Taurine and hypotaurine	metabolism				Glycine, serine and threonine metabolism												
The second secon	GenBank	AccID	1105 AI229235	646 NM_017224	1559 NM_012678	1659 NM 019165	1601 NM 013091	599 NM_013082		1655 NM_017300		493 AF039890	1643 NM_017193	1633 NM 017084		625 A1045440	4624 NIM 04600E	CECOLO MINI	267 AA893552		1446 U05014		1046 AI178828			1512 X73411
	Nucleotide	in indian	1105	1646	1559	1659	1601	1599		1655		493	1643	1633		625	7007	1701	267		1446		1046			1512
	Gl. Gomparison	Code	B,Q	Ø	В	I	B,Q	A,G		⋖		ш	G,H	_ 		_		1301 A,IMI,O	F,G		_		ø			۵
TABLE	25 15	} =	1507 B,Q	1510 Q	1514 B	1520 H	1521 B,Q	1529 A,G		1531		1538 E	1542 G,H	1551 K		1554	7	100	1562 F.G		1571		1572			1570 P

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TABLE	ļ					Nocument Number 1650/75
U	GLGC Comparison	Nuc Sec	GenBank	• "		
	Code	Ω	AccID	Pathways	Known Gene Name	Unigene Cluster Tiffe
				Alanine and aspartate		
				metabolism, Nitrogen		
	1583 A	1448	1448 U07201	metabolism	Asparagine synthetase	Asparagine synthetase
						Rattus norvegicus GADD153 mRNA,
	1598 C,J	1722	1722 NM_024134		DNA-damage inducible transcript 3	complete cds
						Rattus norvegicus survival motor neuron
	1610 C	1703	1703 NM_022509			(smn) mRNA, complete cds
					Cell surface glycoprotein CD44	Cell surface glycoprotein CD44
_		1588	1588 NM_012924		(hyaluronate binding protein)	(hyaluronate binding protein)
					Peptidylglycine alpha-amidating	Peptidylglycine alpha-amidating
_	Ш	1354	1354 E03428		monooxygenase	monooxygenase
					Peptidylglycine alpha-amidating	Peptidylglycine alpha-amidating
	1644 G	208	208 AA891068		monooxygenase	monooxygenase
					Peptidylglycine alpha-amidating	Peptidylglycine alpha-amidating
	1653 G	1222	1222 AI233806		monooxygenase	monooxygenase
				•		Rattus norvegicus inositol
				Inositol phosphate	HHs:inositol polyphosphate-4-	polyphosphate 4-phosphatase mRNA,
	1661 B,E	1459	1459 U26397	metabolism	phosphatase, type I, 107kD	complete cds
						ESTs, Highly similar to MEK binding
-	1690 A,E	46	46 AA817829			partner 1 [M.musculus]
						ESTs, Highly similar to TBB1_RAT
						TUBULIN BETA CHAIN
						[R.norvegicus],Rat mRNA for beta-
	<u>a</u>	1486	1486 X03369		tubulin, beta 2	tubulin T beta15
						Rattus norvegicus zinc finger protein
	1727 C,J	482	482 AF001417			mRNA, complete cds
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Document Number 1650775	Unigene Cluster Title	Rat mRNA for mitochondrial long-chain 3	ketoacyl-CoA thiolase beta-subunit of mitochondrial trif inctional protein.	complete dds	GTP-binding protein		(CYP4F6) mRNA, complete cds	Calcium channel alpha 1A	Cytochrome P450, subfamily IIIA,	polypeptide 3	Cytochrome P450, subfamily IIIA,	polypeptide 3	ESTs	Rattus rattus guanine nucleotide-	releasing protein (mss4) mRNA,	complete cds	Rat mRNA for alpha-2u globulin-related	protein	Protein-tyrosine phosphatase	Protein-tyrosine phosphatase	ESTs, Protein-tyrosine phosphatase	K-kininogen, differential splicing leads to	LIMIM MIGH, I-MIIIIOGGII
	Known Gene Name	HHs:hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme	A thiolase/enoyl-Coenzyme A	subunit	GTP-binding protein	HHs:cytochrome P450, subfamily IVF,	polypeptide 2	Calcium channel alpha 1A	Cytochrome P450, subfamily IIIA,	polypeptide 3	Cytochrome P450, subfamily IIIA,	polypeptide 3							Protein-tyrosine phosphatase	Protein-tyrosine phosphatase	Protein-tyrosine phosphatase	K-kininogen, differential splicing leads	to Hiving Krigk, I -kirillogeri
	Pathways	Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism,	Phenylalanine metabolism,	isoleucine degradation		Prostaglandin and	leukotriene metabolism																
	Nucleotide Sequence GenBank			1332 D16479	1657 NM_017327		1462 U39208	1586 NM 012918		1392 L24207		1392 L24207	47 AA817841			508 A1007824		391 AA946503	1555 NM_012637	1555 NM_012637	1555 NM 012637	7700007	1382 KU2814
TABLE	omparison Code			1728 E.S	. 1749 K		1753 A	1777 P		1795 B,K,Q		1796 B,K	1802 H			1805 N		1809 F	1841 C,N	1843 N,Q	1844 A,N		1854 M

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1495 X51529 48 AA817849 48 AA817377 1013 AI177377 815 AI137856 1397 M10068 1351 E01524
48 AA817849 48 AA817849 013 AI177377 815 AI137856 397 M10068 351 E01524 449 U10357

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Document Number 1650775		Unigene Cluster Title	Hras-revertant gene 107	Rattus norvegicus betaine homocysteine	methyltransferase (BHMT) mRNA,	complete cds	R.norvegicus mRNA for cytosolic	epoxide hydrolase	Solute carrier family 11 member 2	(natural resistance-associated	macrophage protein 2)	Solute carrier family 11 member 2	(natural resistance-associated	macrophage protein 2)	Solute carrier family 11 member 2	(natural resistance-associated	macrophage protein 2)	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	Rattus norvegicus CDK102 mRNA	ESTs, Weakly similar to AF077030_1	hypothetical 43.2 kDa protein	[H.sapiens]	Rattus norvegicus Na-K-Cl cotransporter	(INKCCI) IIIKINA, COIIIDIEIE CUS	ESTs
		Known Gene Name	Hras-revertant gene 107		HMm:betaine-homocysteine	methyltransferase			Solute carrier family 11 member 2	(natural resistance-associated	macrophage protein 2)	Solute carrier family 11 member 2	(natural resistance-associated	macrophage protein 2)	Solute carrier family 11 member 2	(natural resistance-associated	macrophage protein 2)													
		Pathways		Glycine, serine and	threonine metabolism,	Methionine metabolism																-								
	A20 - 11	D Acc ID	628 NM			492 AF038870		1716 NM 022936			1610 NM 013173			1610 NM 013173			1610 NM 013173	721 AI101921	1125 AI230171	417 AA963369	418 AA963372	1084 AI227769	565 AI013667	750 AI103550			423 AA964275		324 AA925961	1475 U75404
	a contraction		X			1995 N		2006 E			2011 P			2012 P			2013 P	2042 Q,R	2043 E.H	2049 J	2051 S	2065	2101 R	2111 A			2113 S		2117 R	2153 F

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Document Number 1650775		Unigene Gluster Title	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	EST	ESTs	ESTs	ESTs, Highly similar to CA14_MOUSE	COLLAGEN ALPHA 1(IV) CHAIN	PRECURSOR [M.musculus]	ESTs	ESTs	EST	ESTs, Highly similar to TGT_HUMAN	QUEUINE TRNA-	RIBOSYLTRANSFERASE [H.sapiens]	ESTs, Highly similar to hypothetical	protein [H.sapiens]	ESTs, Highly similar to JU0227 protein-	tyrosine kinase [M.musculus]	Rattus norvegicus MG87 mRNA,	complete cds	ESTs	ESTs	ESTs	EST	ESTs
		Known Gene Name																													
		Pathways																													
	Nucleotide Seguence GenBank	ID AccID	1223 AI233818	781 AI111413	420 AA964004	776 AI105243	912 A1171745	821 A1144741	421 AA964139	714 AI101362	587 AI029969			432 AA964892	424 AA964302	1162 AI231798	425 AA964336			426 AA964368		454 AA997763		998 AI177029		504 AF095741	1130 AI230373	428 AA964455	429 AA964514	431 AA964752	761 AI104675
TABLE 1	mosilson	Code	꼰	2164 A	2190 S	2196 A	2216 R	2264 A	2280 H	2292 E	2310 M			2326 L	2335 A	2339 E	2342 E			2350 D		2354 L		2359 N		2368 N	2372 A,L	2373 0	2383 A.E	2457 S	2484 A,O

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TABLE 1						Document Number 1650775
		Nucleotide				
010015	Ę	Sequence	Genbank		Variation Course Married	11 Infooms Cinetor Title
П	Code	9	Accilo	Fathways	MIOWII Gene Name	■.
2505 A,G	A,G	1549	1549 NM_012597	Glycerolipid metabolism	Lipase, hepatic	Lipase, hepatic
2506 E	LLJ	524	524 AI009341			ESTs
2532 A	A	975	975 AI176590			ESTs
2536 A	A	978	978 AI176616			ESTs
2555 B,C,Q	3,C,Q	1590	1590 NM 012967		Intercellular adhesion molecule 1	Intercellular adhesion molecule 1
2569 /	2569 A,C,F,K,R	435	435 AA965122			ESTs
2576 A	A	226	226 AA891884			ESTs
2587 G	O	1170	1170 AI232103			ESTs
						ESTs, Moderately similar to Similarity to
2594 L		1241	1241 AI234843			Yeast LPG22P protein [C.elegans]
2615 C.J	L'O	1109	1109 AI229318			ESTs
					Avian myelocytomatosis viral (v-myc)	Avian myelocytomatosis viral (v-myc)
2628		1551	1551 NM_012603		oncogene homolog	oncogene homolog
					Avian myelocytomatosis viral (v-myc)	Avian myelocytomatosis viral (v-myc)
2629		1551	1551 NM_012603		oncogene homolog	oncogene homolog
						Rattus norvegicus protein kinase SNK
2655 B,N,Q	O'Z'S	343	343 AA943886			(Snk) mRNA, complete cds
2667 G	O	1568	1568 NM 012766		Tocopherol transfer protein alpha	Tocopherol transfer protein alpha
2691 R	2	434	434 AA965075			ESTs
						R.norvegicus (Sprague Dawley) mRNA
2696 A	4	1737	1737 NM 022515			for ribosomal protein L24
2727	工	252	252 AA892918			ESTs
Ī					Ca++/calmodulin-dependent protein	Ca++/calmodulin-dependent protein
2736Q		1537	1537 NM 012519		kinase II, delta subunit	kinase II, delta subunit
						ESTs, Highly similar to UGTrel1
2744		1347	1347 D87991			[M.musculus]
2757 [456	456 AA997851			ESTs
2762 A	d	350	350 AA944165			ESTs, Highly similar to C10 [M.musculus]

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Document Number 1650775		Unigene Cluster Title	ESTs	ESTs	Rattus norvegicus mRNA for phocein	protein	ESTs	Rattus norvegicus mRNA for protein	kinase C delta-bindig protein, complete	S	Rattus norvegicus mRNA for protein	kinase C delta-bindig protein, complete	S	ESTs				R.norvegicus mRNA for 3-hydroxy-3-	methylglutaryl CoA lyase	ESTs	ESTs, Highly similar to G7A	[M.musculus]	Cystatin beta	Cystatin beta	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs
		Known Gene Name	ES	ES	Ra	pro	SE	Ra	Kin	cds	Ra	Kin	cds	ES				methylglutaryl-	Coenzyme A lyase me	ES	ES	M]	Cystatin beta Cy	Cystatin beta Cy		ES	ES	ES	ES	ES	<u> </u>
		Pathways													Butanoate metabolism,	Synthesis and degradation	of ketone bodies, Valine,	leucine and isoleucine	degradation												
	GenBank	AccID	1173 AI232269	50 AA817925		939 AI175513	568 AI013778			1345 D85435			1345 D85435	437 AA996451					365 AA945052	1055 AI179144		655 AI070511	1579 NM_012838	1579 NM_012838	1171 AI232209	51 AA818039	603 AI043752	438 AA996727	7 AI030835	439 AA996782	204 AI233288
	Nucleotide on Sequence			2(936	268			134			134	43					36	105		65	157	157	117	5.	09	438	26.	43(120
TABLE 1	GLGC Comparis	ID Code	2763 E	2781 1		2788 J	2799 A			2801 F			2802 F	2803 L				-	2813 S	2818 C,D,F		2838 D	2853	2854	2868 E	2897 C,D	2901 A	2905 A,B	2911 A	2915 R	2932 R

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Document Number 1650775		Unigene Cluster Title	ESTs, Highly similar to beta-site APP	cleaving enzyme [R.norvegicus]	ESTs	ESTs, Highly similar to AF188297_1	TGF-beta receptor binding protein	[M.musculus]	ESTs	EST, Weakly similar to CBPB_RAT	CARBOXYPEPTIDASE B	PRECURSOR [R.norvegicus]	ESTs	ESTs	ESTs	Rattus norvegicus signal transducer and	activator of transcription 1 (Stat1)	mRNA, complete cds	ESTs	ESTs, Highly similar to	NADH:ubiquinone oxidoreductase	NDUFS3 subunit [H.sapiens]	ESTs, Moderately similar to	AF151841_1 CGI-83 protein [H.sapiens]	ESTs	ESTs	ESTs	ESTs	EST	ESTs
		Known Gene Name															HHs:signal transducer and activator of	transcription 1, 91kD		HHs:NADH dehydrogenase	(ubiquinone) Fe-S protein 3 (30kD)	(NADH-coenzyme Q reductase)								
		Pathways																			Oxidative phosphorylation,	Ubiquinone biosynthesis								
	e GenBank			1665 NM_019204	440 AA996883			971 AI176492	885 AI170795			468 AA998857	1213 AI233494	1213 AI233494	1213 AI233494			242 AA892553	1260 AI236027			1113 AI229680		510 AI008160	256 AA893032	1047 AI178850	540 AI010618	1180 AI232408	444 AA997237	447 AA997414
	Nucleotide	Machine Company		166	44			16	38			46	121	121	121			24	126			111		51	25	104	54	118	44	44
—	Compar	ID Code		ш	3 C			× ×	3.6			۵	3073 A.E.O	3074 A,E,O	3075 A,O			<u> </u>	ш	-		S		3121 A.B.E	A	 		3143 E,H	S A	5 5
TABLE 1	29.19	_		2933 E	2938 C			2993 A	3023 G			3062 D	3073	3074	3075			3080 H	3091 E			3099		3127	3131	3138	3139	314	3145 A	3175 S

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Document Number 1650775		Unigene Cluster Title	ESTs, Moderately similar to LDL	receptor member LR3 [M.musculus]	Protein phosphatase 2 (formerly 2A),	catalytic subunit, alpha isoform	ESTs	ESTs, Highly similar to PNAD_MOUSE	PROTEIN N-TERMINAL ASPARAGINE	AMIDOHYDROLASE [M.musculus]	ESTs, Moderately similar to Unknown	gene product [H.sapiens]	Rattus norvegicus fibrillin-1 mRNA,	complete cds	proteasome (prosome, macropain)	subunit, alpha type 5	ESTs	ESTs	ESTs, Weakly similar to putative short-	chain dehydrogenase/reductase	[R.norvegicus]	ESTs	Rat mRNA for contrapsin-like protease	inhibitor related protein (CPi-26)	ESTs	ESTs	ESTs, Highly similar to NHPX_RAT	NHP2/RS6 FAMILY PROTEIN	YEL026W HOMOLOG [R.norvegicus]	Cathepsin L
		Known Gene Name			Protein phosphatase 2 (formerly 2A),	catalytic subunit, alpha isoform									proteasome (prosome, macropain)	subunit, alpha type 5														Cathepsin L
	- Ju	D Pathways		88		039	99			22)5		35		282	5	8			4	6			6	93			5	
THE STATE OF THE S	Nucleotide GenBank			448 AA997438		1624 NM 017039	449 AA997466			767 AI105065		53 AA818105		455 AA997765		1652 NM_017282	571 AI013875	915 AI171948			747 AI103224	1083 AI227699		1325 D00753	518 AI008919	254 AA892993			936 AI175475	1441 S85184
TABLE1	moarison	2000		3189 A		3203 C	3207 A			3219 E		3233 L		3250 M		3253 F	3260 S	3266 L			3279 S	3280 C		3292 M.N	3365 A.B	3381 K			3418 A,C,D	3430 J

Document Number 1650775		Unigene Cluster Title	ESTs, Highly similar to KIAA0564 protein	[H.sapiens]	Rattus norvegicus orphan chemokine	receptor mRNA, complete cds	ESTs	Rattus norvegicus mRNA for R-RCD1,	complete cds	ESTs, Highly similar to ZO1_MOUSE	TIGHT JUNCTION PROTEIN ZO-1	[M.musculus]	choline/ethanolamine kinase	Rat signal peptidase mRNA, complete	cds	EST	ESTs, Weakly similar to RET1_RAT	RETINOL-BINDING PROTEIN I,	CELLULAR [R.norvegicus]	ESTs	:	Rattus norvegicus gene for	hepatocarcinogenesis-related	transcription factor (HTF), complete cds	ESTs, Weakly similar to JC1450	fibroblast growth factor receptor 4 - rat	[R.norvegicus]	ESTs, Highly similar to Opa-interacting	protein OIP2 [H.sapiens]	ESTs	EST
		Known Gene Name											choline/ethanolamine kinase																		
		Pathways											Glycerolipid metabolism																		
	SenBank			255 AA893000		452 AA997721	869 AI170313		760 AI104659			963 AI176423	1639 NM 017177		1385 L11319	463 AA998461			464 AA998510	1078 AI180253				1259 AI236021			950 AI176031		302 AA924460	467 AA998833	469 AA999060
	Nuc			255		452	869)92			:96 	1638		138	46;			46	1078				1259			95(30:	46	46
TABLE 1	GLGC Comparison	ID Code	-	3439 S		3452 M,N	3486 H		3504 A.B			3510 K	3513 S		3549 H,I	3558 S			3570 0	3587 J				3617 N			3626 P		3631 S	3660 B	3708 M

Document Number 1650775	er est	Unigene Cluster Title	ESTs	ESTs	ESTs	ESTs	EST	Rat mRNA for brain acyl-CoA	synthetase II, complete cds	EST	Uncoupling protein 2, mitochondrial	Rattus norvegicus 250 kDa estrous-	specific protein mRNA, partial cds	ESTs, Highly similar to PSD5_HUMAN	26S PROTEASOME SUBUNIT S5B	[H.sapiens]	ESTs, Weakly similar to nuclear RNA	helicase [R.norvegicus]	ESTs, Weakly similar to nuclear RNA	helicase [R.norvegicus]		R.norvegicus mRNA for vacuolar	adenosine triphosphatase subunit B	ESTs, Weakly similar to similar to acyl-	CoA dehydrogenases and epoxide	hydrolases [C.elegans]	ESTs, Moderately similar to CGI-147	protein [H.sapiens]	ESTs	ESTs	ESTs
		Known Gene Name									Uncoupling protein 2, mitochondrial										HMm:ATPase, H+ transporting,	lysosomal (vacuolar proton pump), beta R.norvegicus mRNA for vacuolar	56/58 kDa, isoform 2								
The part of the property of the part of th		Pathways																,					Oxidative phosphorylation								
	Jungang	Acc ID	470 AA999064	791 AI112571	471 AA999138	457 AA997979	460 AA998234		1335 D30666	461 AA998276	1679 NM_019354		884 AI170773			1219 AI233729		288 AA900863		1196 AI233147			1525 Y12635			658 AI070895		567 AI013745	865 AI169947	1194 AI232970	270 AA894233
A CONTRACTOR OF THE CONTRACTOR		D	470	791	471	457	460		1335	461	1679		884			1219		288		1196			1525			658		292	865	1194	270
		ID Code	B,Q	A,N	S	z	z		တ	Ь	g		L,R			•		⋖		⋖			C,J			0		٧	A,F	В	0
TABLE			3710 B,Q	3713 A,N	3720 S	3722 N	3730 N		3743 S	3749 P	3776 Q		3803 L,R			3816		3822 A		3823 A			3831			3846 0		3849 A	3916 A,F	3917 B	3929 O

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Document Number 1650775		Unigene Cluster Title	ESTs	ESTs	ESTs, Weakly similar to 137195 AU-	specific RNA-binding protein / enoyl-CoA	hydratase [H.sapiens]	Rat beta-galactoside-alpha 2,6-	sialyltransferase mRNA	ESTs, Weakly similar to JC5105 stromal	cell-derived factor 2 - mouse	[M.musculus]	Rat sperm membrane protein (YWK-II)	mRNA, 3' end	Rattus norvegicus late gestation lung 2	protein (Lgl2) mRNA, complete cds	Rattus norvegicus mRNA for AIF-C1,	complete cds	ESTs	ESTs, Moderately similar to	AF153605_1 androgen induced protein	[H.sapiens]	ESTs, Moderately similar to	AF153605_1 androgen induced protein	[H.sapiens]	selenoprotein P, plasma, 1	Rattus norvegicus peroxisomal	ESTS
		Known Gene Name				S	u	alactoside	alpha-2,6-sialytransferase)		0			ı.				0	3				3	_		selenoprotein P, plasma, 1		
		S Pathways																										
	Nucleotide Seguience Can Bank		170 AA859536	1132 AI230431			923 AI172274		1425 M83143			371 AA945591		1415 M31322		1159 AI231763		1685 NM 021577	76 AA818700			321 AA925603			1152 AI231309	1663 NM_019192	4000 A 0004	79 AA818741
TABLE1	omosricon	D Code	4178	4179 A,C,E,R			4193 A,C,D,E,F,I		4199 G			4207 F		4224 G		4231 R		4234 H	4250 B			4271 S			4272 S	4281 A,G	000	4290 S

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Document Number 1650775	Venum Cone Name	Rattus no	carboxylesterase precursor, complete	spo	Rattus norvegicus bile salt export pump	(spgp) mRNA, complete cds	Rattus norvegicus mRNA for endothelial	receptor for oxidized low-density	lipoprotein, complete cds	Rattus norvegicus nuclear RNA helicase	mRNA, complete cds	Rattus norvegicus stromal cell-derived	factor-1 gamma mRNA, complete cds	Rattus norvegicus mRNA for	norepinephrine transporter b (rNETb),	complete cds	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	Rattus norvegicus DOC-2 p59 isoform	mRNA, complete cds	HHs:NADH dehydrogenase ESTs, Moderately similar to NADH-		ESTs	ESTs
		Fallways																			-				noite/randraoda ovitebixO			
	GenBarrk	Accilu		480 AB010635		483 AF010597			474 AB005900		498 AF063447		80 AA818747			874 AI170447	1358 H31813	295 AA924196	3 AA685974	2 AA684919	1189 AI232643	229 AA891965		1725 NM 024159		751 AI103694	999 AI177038	1049 AI178872
	Nuc	2		480		483			474		498		80			874	1358	295	3	2	1189	229		1725		751	666	1049
		apo^		<u>×</u>		4314 G,M			Щ				4330 A.C.D.E			Ш	<	Ш		S	A,O	4		œ		0	A,C	\
TABLE	2979	2		4312 K		4314			4318	2	4327		4330			4348 E	4360 A	4371	4426	4438 S	4440 A.O	4473 A		4504 Q		45200	4553 A.C	4576 K

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Document Number 1650775	Known Gene Name	Rattus norvegicus mRNA for phosphoinositide 3-kinase, complete cds	eukaryotic translation initiation factor 2, eukaryotic translation initiation factor 2, subunit 1 (alpha)	ESTs	ESTs	ESTs	EST	ESTs, Highly similar to IRF3_MOUSE INTERFERON REGULATORY FACTOR	3 [M.musculus]	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	EST	ESTs, Moderately similar to unknown	[H.sapiens]	EST	ESTs	Rattus norvegicus rap7a mRNA, complete cds	
	Pathways																							
	GenBank Acc ID	477 AB009636	1680 NM 019356	1075 AI179991	718 AI101582	1217 AI233714	279 AA899847		585 AI029847	1087 AI228265	282 AA900290	285 AA900553	1228 AI233925	752 AI103708	882 AI170763	611 AI044292	785 AI112086	296 AA924236		297 AA924261	299 AA924301	1294 AI237189	1738 NIM 000506	ININI_UZEOZEO
	Nucleotide Sequence ID	477	1680	1075	718	1217	279		585	1087	282	285	1228	752	882	611	785	296		297	299	1294	1738	30 1 -
TABLE 1	GLGC Comparison	4588 K	4592 C.D	4610 E	4650 G	4670 A,N	4674 O		4679 L	4719 A	4725 L	4759 E	4781 C,D	4856 1	4868 A	4892 P	4914 A	4929 E		4931 S	4933 A.E.P	4937 A.L	0.000	4940 5

Document Number 1650775		Unigene Cluster Title	ESTs, Moderately similar to	NO56_HUMAN NUCLEOLAR PROTEIN	NOP56 [H.sapiens]	ESTs	ESTs	ESTs, Moderately similar to	megakaryocyte stimulating factor	[H.sapiens]	ESTs	EST	ESTs, Weakly similar to MRJ	[M.musculus]	ESTs	ESTs	ESTs	ESTs, Weakly similar to TTHY_RAT	TRANSTHYRETIN PRECURSOR	[R.norvegicus]	ESTs	ESTs	ESTs	EST,ESTs				Pyruvate kinase, muscle	ESTs	ESTs, Moderately similar to BcDNA.GH02974 [D.melanogaster]
		Known Gene Name																										Pyruvate kinase, muscle		
		Pathways																7							Glycolysis/	Gluconeogenesis, Purine	metabolism, Pyruvate	metabolism		
	GenBank	AccID			301 AA924405	519 AI009026	86 AA818907			795 AI113008	88 AA818921	306 AA924767		307 AA924768	308 AA924793	846 AI169239	303 AI237855			1270 AI236302	1288 AI236947	699 AI073092	317 AA925274	397 AA955729				90 AA818951	322 AA925807	829 A1145569
	Nucleotide Sequence				301	519	98			795	88	306		307	308	846	1303			1270	1288	669	317	397				06	322	829
_	GLGC Comparison	Code			A,F	A	C,J			Σ	A,C			Ш	A	Ш	A,L			2	Ø	E	E,M	Ш				⋖	A	L.
TABLE	2979	Ω			4944 A,F	4951 A	4952 C,J			4969 M	5008 A,C	5018		5020 E	5027 A	5038 E	5046 A,I		•	5052 R	5059 Q	5091 E	5110 E,M	5111		-		5175 A	5219 A	5235 F

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Document Number 1650775		Unigene Cluster Title	ESTs	ESTs, Moderately similar to	SYQ_HUMAN GLUTAMINYL-TRNA	SYNTHETASE [H.sapiens]	ESTs, Weakly similar to PNMT	ase [R.norvegicus]	ESTs	ESTs		Rat proopiomelanocortin (POMC) gene	ESTs	EST	ESTs, Highly similar to AF172275_1	FUS2 [M.musculus]	ESTs	illy, ESTs,UDP-glucuronosyltransferase 1 family, member 1	
		Known Gene Name				HHs:glutaminyl-tRNA synthetase		HMm:nicotinamide N-methyltransferase [R.norvegicus]			Proopoimelanocortin, beta (endorphin,	beta)						UDP-glucuronosyltransferase 1 family, member 1	member 1
		Pathways		Aminoacyl-tRNA	biosynthesis, Glutamate	metabolism	Nicotinate and nicotinamide	metabolism										Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose	metabolism
	Nucleotide Sequence GenBank					91 AA818996		911 AI171727	1038 AI178734	207 AA891041		1380 K01878	407 AA956910	613 AI044338		614 AI044345	914 AI171795	1336 D38061	1433 S56936
TARI F1	omparison	ID Code	5291 M			5331		5339 E,M	5381 R	. 5384 A,B,F		5434 E	5437 F	5461 A		5464 B,O	5489 C,J	5492 G	5493 G,O

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Document Number 1650775		. Unigene Cluster Title	ESTs, Weakly similar to NUML_MOUSE	NADH-UBIQUINONE	OXIDOREDUCTASE MLRQ SUBUNIT	[M.musculus]	EST	ESTs	ESTs, Weakly similar to mitochondrial	very-long-chain acyl-CoA thioesterase	[R.norvegicus]	ESTs	Fibronectin 1	Fibronectin 1	ESTs	ESTs	0.5	P-glycoprotein/multidrug resistance 1	ESTs, Moderately similar to	DYNC_HUMAN DYNACTIN, 50 KD	ISOFORM [H.sapiens]	proteasome (prosome, macropain)	subunit, alpha type 2	proteasome (prosome, macropain)	subunit, alpha type 2	ESTs	ESTs, Weakly similar to DRAL	[R.norvegicus]	ESTs	ESTs
		Known Gene Name											Fibronectin 1	Fibronectin 1			P-glycoprotein 2/ multidrug resistance	ID,F-glycoploteii/illiditidi.ug resistarice 1				proteasome (prosome, macropain)	subunit, alpha type 2	proteasome (prosome, macropain)	subunit, alpha type 2					
		Pathways																												
	e GenBank					1165 AI231805	617 AI044550	377 AA945879			1187 AI232611	93 AA819041	1731 NM_019143	1731 NM_019143	705 AI101006	621 AI045116		1424 M81855			680 AI072092		1650 NM_017279		1650 NM_017279	133 AA850738		1019 AI177869	1212 AI233480	626 Al045441
	Nucleotide					116	61	37			118	6	173	173	02	62		142			89		165		165	13		101	121	62
-	Gl.GC Comparison	Code				<u></u>	S	S			S	R	5616 M,S	A	Ь			ن					₹		5749 A,H	5754 L,R		5780 C,D	O	Ш
TABLE	08.18	9				5504	5518	2565 S			5602 S	5608 R	5616	5622 A	5687 P	2696		5733 C			5740		5748 A		5748	5754		5780	5794 C	5795 E

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Document Number 1650775		Known Gene Name Unigene Cluster Title	ESTs	ESTs	EST	ESTs	ESTs, Highly similar to SYN_HUMAN ASPARAGINYL-TRNA SYNTHETASE,	HHs:asparaginyl-tRNA synthetase CYTOPLASMIC [H.sapiens]	protein	ESTs, Moderately similar to Vanin-1	[M.musculus]	ESTs	ESTs	ESTs	ESTs, Moderately similar to M phase	phosphoprotein 10 [H.sapiens]	ESTS	ESTs	ESTs, Highly similar to 2008147C	protein KAKa [K.norvegicus]	ESTs	ESTs	Rattus norvegicus amino acid	transporter system A (ATA2) mRNA,	complete cds	ESTs	ESTs	ESTs	ESTs
		Market State of State						HHs:asba			vanin 1																		
		Pathways					Alanine and aspartate metabolism. Aminoacvi-	tRNA biosynthesis																					
4.0	GenBank	Acc ID	1026 AI178231	1285 AI236771	627 AI045555	95 AA819111		158 AA858953	1322 AJ223184		1053 A1179099	867 AI170038	843 AI169163	65 AA818355		1017 AI177638	42 AA817688	756 AI104254		43 AA817695	908 AI171684	1005 AI177105			893 AI171231	89 AA818947	820 AI144612	1317 AI639501	54 AA818107
	Nucleotide Sequence	9	1026 A	1285 A	627 A	95 A		158 A	1322 A		1053 A	867 A	843 A	65 A		1017 A	42 A	756 A		43 A	908 A	1005 A			893 A	A 68	820 A	1317	54 4
7	Comparison	Code		n	×	A		A.C.D			S	A,D,F	Ð	A			Ш	ſ		A,F		A			I	I	2	9	Ш
TABLE 1	OE) IE	₽	5813 A	5820 J	5824	5863 A		5867 A.C.D	5885		5887 S	5899 A,D,F	5920	5923 A		5926 C	5930 E	5932		5934 A,F	5937	5943 A			5953 H	2966 H	5993 R	5998 G	6003 E

Document Number 1650775	The London Colonia Sept.		2 2 3	ESTs	C-reactive protein	ESTs	EST	carbonic anhydrase 3	carbonic anhydrase 3	EST	ESTs	ESTs	ESTs	ESTs, Highly similar to HN1	[M.musculus]	ESTs	ESTs	ESTs, Weakly similar to Similarity to	litosperm LEC14B protein [C.elegans]	ESTs, Moderately similar to axonemal	dynein heavy chain [H.sapiens]	ESTs	EST	ESTs, Moderately similar to selenium-	binding protein [H.sapiens]	EST	Rattus norvegicus pro-alpha-2(I)	collagen (col1a2) mRNA, complete cds	Rattus norvegicus pro-alpha-2(I)	collagen (col1a2) mRNA, complete cds	ESTs
		Nnown Gene Name	The second section of the second seco		C-reactive protein			carbonic anhydrase 3	carbonic anhydrase 3																						
		Patnways						Nitrogen metabolism	Nitrogen metabolism																						
	tide nce	ID Accilo	55 AA818123	56 AA818139	1634 NM_017096	57 AA818158	58 AA818163	1676 NM_019292	96 AA819140	59 AA818211	60 AA818258	1195 AI233081	64 AA818288		330 AA942716	77 AA818702	83 AA818781		1093 AI228630		916 AI171990	881 AI170752	94 AA819055		771 AI105167	98 AA819199		203 AA875531		715 AI101443	82 448774
TABLE1	omparison	ID Code	6007 A	6012 D	6013 N	6015 A,O	6016 A,C,D	6017 A	6018 E,N	6026 E	6032 E	6033 A	6037 A		6039 D	6060 A,O	9009 E		6072 A,B,E,F		6085 C	6101 R	6132 A,C,D		6143 A.C	6151 G		6153 G		6155 G	£188 □

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Document Number 1650775		Unigene Cluster 1 file	ESIS, Weakly similar to GIP_KAI	GLUTATHIONE S-TRANSPERASE P	[K.norvegicus]	ESTs	ESTs	ESTs	ESTs, Highly similar to TNFC_MOUSE LYMPHOTOXIN-BETA [M.musculus]	ESTs	ESTs	ESTs	EST, Moderately similar to ISI1_RAT	INSULIN-INDUCED PROTEIN 1	[R.norvegicus]	ESTs. Weakly similar to B39066 proline-	rich protein 15 - rat [R.norvegicus]	ESTs	ESTs	EST	ESTs, Weakly similar to AIF-C1	[R.norvegicus]	EST	ESTs	Rattus norvegicus mRNA for signal	peptidase 21kDa subunit, complete cds	ESTs, Weakly similar to dJ413H6.1.1	[H.sapiens]
		Known Gene Name							HHs:lymphotoxin beta (TNF superfamily member 3)																			
	h.	Pathways														•												
	ide ce GenBank	Acc ID			1023 AI178027	107 AA819812	1161 AI231797	109 AA819840	110 00810853	726 AI102190	68 AA818474	70 AA818521			75 AA818627		875 AI170617	822 AI144797	422 AA964181	103 AA819672		712 AI101256	85 AA818801	873 AI170426		152 AA858716		153 AA858758
	Nucleotide Comparison Sequence	Code													<u>م</u>													Q';
TABLE 1	00 2919	9			6189 B,E,G	6190 A	61931	6198 M	0000	6213 N	6222 N	6226 A			6236 B,E,P		6272 L	6291 H	6292 S	6295 N		6321 A,J	6322 A	6330 H		6366 A.E.H		6380 A,C,D

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	Annana	-4.		
ID Code ID	AccID	Pathways	Known Gene Name	Unigene Cluster Title
156	156 AA858910			ESTs
157	157 AA858926			ESTs
159	159 AA859085			EST
989	636 AI058436			ESTs
160	160 AA859130			ESTs
161	161 AA859150			ESTs
1002	1002 AI177091			ESTs
1371	1371 J00735		Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide
1098	860 AI169690		Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide
1232	1232 AI234105			ESTs
				ESTs, Moderately similar to hypothetical
155	155 AA858852			protein [H.sapiens]
740 /	740 AI102905			ESTs
				ESTs, Highly similar to S65755
				tetrahydrofolylpolyglutamate synthase
949	949 AI176002	Folate biosynthesis	Folylpolyglutamate synthase	[M.musculus]
594	594 AI030271			ESTs
505	505 AF097723			Rattus norvegicus liver annexin-like protein (LAL) mRNA, complete cds
				ESTs, Weakly similar to ESR1_RAT
910	910 AI171726			ESTROGEN RECEPTOR [R.norvegicus]
				Rattus norvegicus mRNA for connective
1695	1695 NM_022266			lissue growiii lactor, corriptete cus
1104	1104 AI229192			ESTS

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Document Number 1650775	Unigene Cluster Title	Raftus norvegicus L-3-hydroxyacyl-CoA	dehydrogenase precursor (HAD) mRNA, complete cds; nuclear gene for	FSTs Weakly similar to putative type III	alcohol dehydrogenase	[D.melanogaster]	ESTs	ESTs	ESTs	ESTs	Rattus norvegicus mRNA for N-cadherin,	complete cds	ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to methyl-CpG	binding domain-containing protein MBD3	[M.musculus]	ESTs	ESTs	ESTs	ESTs	ESTs
	Known Gene Name		HMm:hydroxylacyl-Coenzyme A	denydrogenase																				
	Pathways	Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation,	Tryptophan metabolism, Valine, leucine and	Isoleucine degradation																				
	GenBank Acc ID			117 AA848758		335 AA942889	1246 AI235277	1098 AI228931	716 AI101500	905 AI171646		612 AI044325	143 AA851967	542 AI011471	1168 AI232065	952 AI176130			513 AI008699	459 AA998207	735 AI102753	857 AI169619	536 AI010316	509 AI007877
	Nucleotide Sequence ID			117		335	1246	1098	716	902		612	143	542	1168	952			513	459	735	857	536	209
	GLGC Comparison			A,F		۷_	A	A,N	A	ᅩ		ш		S	A	K.			٨	O,R	U	Ш	6801 A,E,K	Ш
TABLE 1	GI Celec			6613 A,F		6615 A	6632 A	6633	6640 A	6667 K		6673 E	19299	8 2 2 9 S	6682 A	6686 R			6761	6789 O,R	2 96 C	6798 E	6801	6804 E

TOTATION NOT TOTAL

Document Number 1650775	ا الله . " Unigene Cluster Title. الله الله الله الله الله الله الله الل	EST, Rattus norvegicus Mdk mRNA for	midkine, complete cds	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	Rattus norvegicus DnaJ-like protein	(RDJ1) mRNA, complete cds		Rattus norvegicus mRNA tor	dihydropyrimidine dehydrogenase,	_	ESTs	ESTs	ESTs, Weakly similar to Dreg-2 protein	[D.melanogaster]	ESTs, Weakly similar to TERA_RAT	TRANSITIONAL ENDOPLASMIC	RETICULUM ATPASE [R.norvegicus]	ESTs			Aldolase A, fructose-bisphosphate
	Known Gene Name													-		HHs:dihydropyrimidine dehydrogenase											Aldolase A, fructose-bisphosphate
	Pathways												Pantothenate and CoA	biosynthesis, Pyrimidine	metabolism,beta-Alanine	metabolism					-				Fructose and mannose	Gluconeogenesis, Pentose	phosphate cycle
	Q aorientes		717 AI101534	1133 AI230439	990 A1176841	104 AA819709	631 AI045972	899 AI171370	995 AI176970	907 A1171674		33 AA800551				1343 D85035	537 AI010461	953 AI176229		593 A1030259			1164 AI231801	543 AI011503			1533 NM_012495
TABLE	GLGC Companson		6814 E	6820 A.D	6821 E.L	6824 A.C.D.F.I	6825 A.B.Q.S	6855 A.L	6861 H.R	6879		6892 J				6911 D	6919 N	6975 0		7003 4 1			7036 C.1	7056 B,M			7062 A

Document Number 1650775	Unigene Clüster Title	Aldolase A, fructose-bisphosphate	Aldolase A. fructose-bisphosphate	ESTs	ESTs	ESTs	ESTs	ESTs	Annexin 1 (p35) (Lipocortin 1).	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to CIRP	[R.norvegicus]	ESTs	ESTS, Weakly similar to AF165892_1	[R.norvegicus]	ESTs	EST
	Known Gene Name	Aldolase A, fructose-bisphosphate	Aldolase A fructose-bisphosphate						Annexin 1 (p35) (Lipocortin 1)													
	Pathways	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose phosphate cycle	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose																			
	Nucleotide SenBank Sequence GenBank ID Acc ID	1533 NM 012495	1533 NM 012495	108 AA819816	868 AI170260	809 AI137468	1209 AI233407	1306 AI639029	1585 NM_012904	562 Al013044	564 AI013657	1218 AI233717	946 AI175833	1115 AI229739	572 AI013876		573 AI013911	111 AA819854		577 AI028973	578 AI029026	579 AI029212
TABLE1	GLGC Comparison ID Code	3 A C	7064	7111 R	7113 A	7122 Q	7161 C	7176 Q	7196 P	7199 C,D	7225 M	7243 A,C	7262 D,L	7271 C	7295 S		7299 A	7301 J		7352 A	7362 L	7403 C.D

Document Number 1650775		Unigene Cluster Title	ESTs, Highly similar to IMB3_HUMAN	IMPORTIN BETA-3 SUBUNIT	[H.sapiens]	ESTs, Highly similar to ClpX-like protein	[H.sapiens]	ESTs, Moderately similar to	SYEP HUMAN MULTIFUNCTIONAL	AMINOACYL-TRNA SYNTHETASE	[H.sapiens]	ESTs, Moderately similar to	sphingomyelin phosphodiesterase 1,	acid lysosomal [H.sapiens]	ESTs	ESTs, Highly similar to AF115778_1	short coiled coil protein SCOCO	[M.musculus]	ESTs	ESTs	EST	ESTs	ESTs	ESTs	Rattus norvegicus mRNA for of CBP-50	protein	ESTs	ESTs	ESTs, Moderately similar to	methyltransferase related protein	[M.musculus]
		Known Gene Name											HMm:sphingomyelin	phosphodiesterase 1, acid lysosomal																	
		Pathways											Sphingophospholipid	biosynthesis				•													
	GenBank	AcciD			813 AI137586		580 AI029291				581 AI029450			849 AI169302	582 AI029709			749 AI103548	1298 AI237614	584 AI029829	629 AI045802	588 AI029996	601 AI043724	589 AI030024		1320 AJ001929	591 AI030170	596 AI030668			595 AI030449
	Nucleotide				813		280				581			849	582			749	1298	584	629	588	601	589		1320	591	596			262
•	Comparison	Code			CD		<u>.</u>				Z			<u> </u>	S			I	Δ		F.G.I	Y A	0			wine.	A	L			A
TABLE	2012	} }	i.		7414		7420 S				7451 F N	2		7497	7517 S			7528 H	7531 A	7537 F	7552 F G	7582 A	7584	7586	3	7602	7617	7665 F			7681 A

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Document Number 1650775		unigene Cluster Title	ESTs	Rattus norvegicus uroguanylin mRNA,	complete cds	ESTs	ESTs	Dipeptidyl peptidase 4	Dipeptidyl peptidase 4	ESTs	EST	ESTs	ESTs, Moderately similar to	SYR_HUMAN ARGINYL-TRNA	SYNTHETASE [H.sapiens]	ESTs, Moderately similar to	SYR_HUMAN ARGINYL-TRNA	SYNTHETASE [H.sapiens]	ESTs, Weakly similar to FIBA_RAT	FIBRINOGEN ALPHA/ALPHA-E CHAIN	PRECURSOR [R.norvegicus]	EST	ESTs	`	ESTs, Highly similar to sterol-C5-	desaturase [M.musculus]	ESTs	R.norvegicus mRNA for UDP-N-acetyl-D	glucosamine-2-epimerase
		Known Gene Name						Dipeptidyl peptidase 4	Dipeptidyl peptidase 4						HHs:arginyl-tRNA synthetase			HHs:arginyl-tRNA synthetase						HMm:sterol-C5-desaturase (fungal	ERG3, delta-5-desaturase) homolog (S. ESTs, Highly similar to sterol-C5-	cerevisae)		HHs:UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine	kinase
	-re-1 c c c c c - 2 c - 2	Pathways											Aminoacyl-tRNA	biosynthesis, Arginine and	proline metabolism	Aminoacyl-tRNA	biosynthesis, Arginine and	proline metabolism								Sterol biosynthesis			Aminosugars metabolism
	GenBank	Acc ID	592 AI030242		1700 NM_022284	992 AI176942	651 AI070233	1570 NM 012789	1570 NM_012789	67 AA818421	599 AI043654	711 AI101229			823 AI144832			1215 AI233583			1102 AI229172	604 AI043761	605 AI043805			606 AI043855	1069 AI179750		831 AI145931
	Nucleotide Sequence	a	592		1700	992	651	1570	1570	29	299	711			823			1215			1102	604	605			909	1069		831
_	Nucleotide GLGC Comparison Sequence	Code	0			A,M	۵	A	A,C	J	M,P	A			C.D			7888 A.C.D			Ш	A	A.E.F			ш	A		7927 A,H,O
TABLE	2979	<u></u>	7684 0		10697	7697 A,M	7743 P	7784 A	7785 A,C	7806	7858 M.P	7868 A			7887 C.D			7888			7892 F	7893 A	7903 A.E.F			7916 E	7918 A		7927

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Document Number 1650775	Unigene Cluster Title	ESTs	ESTs	ESTs	EST, Weakly similar to putative integral	membrane transport protein [R.norvegicus]	ESTs	ESTs	ESTs	ESTs, Moderately similar to PROP MOUSE PROPERDIN	[M.musculus]		ESTs	Rattus norvegicus protein-tyrosine	phosphatase (SHP-1) mRNA, complete	cds	ESTs	ESTs	Rat ferritin light chain subunit,	mRNA,Rattus norvegicus kynurenine	aminotransferase/glutamine	transaminase K (Kat) gene, complete	cds	ESTs	EST, Weakly similar to hypothetical	protein [H.sapiens]	ESTs
	Known Gene Name	HMm:ferrochelatase		HHs:adenylate cyclase 9								Protein tyrosine phosphatase, gamma	(provisional HGM11 symbol)			HMm:hemopoietic cell phosphatase											
	i Pathways	Porphyrin and chlorophyll metabolism		Purine metabolism																		,					
	GenBank Acc ID	607 AI043945	202 AA875495	1124 AI230134		633 Al058341	932 AI175033	1099 AI228959	637 AI058581		1318 AI639534		742 AI103071			1478 U77038	450 AA997699	638 AI058603					909 AI171692	765 AI104908		641 AI059270	1048 AI178868
	Nucleotide m Sequence ID		202	112		633	937	1099	63		1318		74.			1478	45(928					306 —	76		. 64	104
E1	GLGC Comparison ID Code	7935 C	6 A	7 L		<u>d</u> 2	3 K	4 R	8079 B,M,Q		2 <u>C</u>		4 E			2	3 E	7.8					5 L	3 P		4 B	0 P
TABLE	ore ore	793	7936 A	7967		8017 P	8053 K	8054 R	807		8107		8124			8152	8173 E	8177 S					8215	8273 P		8274 B	8310 P

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Document Number 1650775	Unigene Cluster Title	ESIS	ESTs, Highly similar to PUA1_MOUSE ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME [M.musculus]	ESTs, Moderately similar to microsomal glutathione S-transferase 3 [H.sapiens]	EST	ESTs	ESTs	ESTs	ESTs	ESTs	Rattus norvegicus sterol delta 8- isomerase (RSI) mRNA, complete cds	Rattus norvegicus phosphatidate	phosphohydrolase type 2 mRNA,	complete cds	ESTs	ESTs	Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds	Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds	Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
	Known Gene Name		HMm:adenylosuccinate synthetase 1, muscle	HHs:microsomal glutathione S- transferase 3													Heat shock protein 70-1	Heat shock protein 70-1	Heat shock protein 70-1
	Pathways		Alanine and aspartate metabolism,Purine metabolism	Glutathione metabolism											-				
	nice GenBank Acc ID	642 AI059386	643 AI059389	234 AA892234	645 AI059543	962 AI176365	1056 AI179167	127 AA849917	647 AI060071	1216 AI233639	1364 H33491			72 AA818593	640 AI058956	529 AI009677	73 AA818604	115 448563	1527 727118
	GLGC Comparison Sequence ID Code ID			<u>س</u>	-			-	A,P	I				В.Н					
TABLE	ם בפר כ	8314 J	8315 S	8317 A.E	8356 G	8387 A	8477 A	8515 N	8522 M,P	8549 A.F.H	0507	2500		8597 B	8600 A	8630 A	8661	6998	8663

Document Number 1650775		Unigene Cluster Title	ESTs, Rattus norvegicus heat shock	protein 70 (HSP70) mRNA, complete	cds	ESTs, Rattus norvegicus heat shock	protein 70 (HSP70) mRNA, complete	spo	ESTs, Weakly similar to putative	peroxisomal 2,4-dienoyl-CoA reductase	[R.norvegicus]	ESTs	ESTs, Weakly similar to DnaJ homolog 2	[R.norvegicus]	ESTs	ESTs	ESTs	Rattus norvegicus clone Pr2 unknown	mRNA	ESTs, Weakly similar to thyroid hormone	responsive protein [R.norvegicus]	ESTs	Nucleolin	ESTs	ESTs	ESTs	ESTs, Highly similar to Ki antigen	[M.musculus]	ESTs	ESTs
		Known Gene Name			Heat shock protein 70-1			Heat shock protein 70-1															Nucleolin							
		Pathways																												
	GenBank	Acc ID			1530 275029			675 AI071965			610 AI044247	634 AI058388		1185 AI232534	648 AI069920	74 AA818615	1028 AI178483		697 AI073047		549 AI012085	650 AI070152	1567 NM 012749	652 AI070319	134 AA851050	824 AI144936		1221 AI233766	790 AI112511	212 AA891221
	Nucleotide Sequence				1530			675			610	634		1185	648	74	1028		269		549	029	1567	652	134	824		1221	790	212
	Comparison	Code						_			4	E,M		ď	z	2			I		∢	S	4	Ь	G.K	A		٥	×	
TARIF1	20 10	9			8664	3		8665			8692	8700 E,M		8709 R	8715 N	8728 R	8730 H	3	8735 H		8766 A	8820 S	8829 A	8864 P	8872 G.K	8880		G 9888	8905 K	8928

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Document Number 1650775	nBank Pathways Known Gene Name Unigene Cluster Title	ESTS	HSp::METHIONINE AMINOPEPTIDASE	2		0879 EST	4810 ESTs								Spinocerebellar ataxia type 1		6947 ESTs	9870 ESTs		ALPHA-HYDROXYSTEROID	2107 DEHYDROGENASE [R.norvegicus]	7345 ESTs	Rat MHC class II RT1.B beta gene,	encoding cell surface glycoprotein beta	chain, Rat mRNA for MHC class II	antigen RT1.B-1 beta-chain,Rattus	151 beta chain mRNA, partial cds
	GenBank Acc ID	656 AI070611		1735 NM_022539	948 AI175997	657 AI070879	239 AI234810	659 AI070903	AA892861	1197 AI233162	942 AI175635	667 AI071251	903 AI171611	516 AI008813	NM 012726	807 AI137406	993 AI176947	1071 AI179870	702 AI100835		AI072107	805 AI137345				•••	1417 M36151
	Nucleotide mparison Sequence			1735	948	657	1239	C,D,E 659	249	1197	942	299	803	516	1565	807	993	1071	702		681	802					1417
TABLE 1	5	A		8984 J	8993 R	9012 A	9015 K	B	9053 A	9063 A	9072 G	9079 P	9128 L	9148 B	9164 H	9166 E	9170 E	9181 C,D	9190 H		9191 A	9192 E					9223

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Document Number 1650775		Unigene Cluster Title	ESTs	ESTs, Moderately similar to human	formiminotransferase cyclodeaminase	[H.sapiens]	ESTs, Moderately similar to SPIN	[H.sapiens]	ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to CDN6_MOUSE	CYCLIN-DEPENDENT KINASE 6	INHIBITOR [M.musculus]	ESTs	ESTs	Ryudocan/syndecan 4	Ryudocan/syndecan 4	Ryudocan/syndecan 4	EST	ESTs	ESTs	Rat rhoB gene mRNA, complete cds	ESTs	ESTs	ESTs	ESTs	ESTs	Rat PRRHIS8 mRNA for ribosomal	protein S8
		Known Gene Name																Ryudocan/syndecan 4	Ryudocan/syndecan 4	Ryudocan/syndecan 4											ribosomal protein S7
	21	Pathways																													
	otide GanBank		684 AI072278			685 AI072384		799 AI136514	689 AI072633	691 AI072643	692 AI072712	802 Al136714		. •	854 AI169557	693 AI072812	101 AA819383	1556 NM_012649	1556 NM_012649	27 AA800059	695 AI072914	698 AI073059	69 AA818490	1704 NM 022542	660 AI071162	664 AI071185	800 AI136630	1365 H33832	666 AI071227		937 AI175486
	Comparison Sections	ID Code ID				Ø		A	9331 A,C,D	А	S	S			~	A	9402 O,R	S	Z	A	ш	9475 A,O		A	2	A	9595 B,E,Q	Ш	Ш		0
TABLE	100		9245 A			9267		9326 A	9331	· 9336 A	9372	9373 S			9374 R	9399	9405	9423 S	9424 N	9425 A	9432	9475	9486	9541 A	9572 R	9583 A	9595	9598 E	9603 E		9621

Document Number 1650775	Unigene Cluster Title	ESTs	ESTs, Weakly similar to Y281_HUMAN	HIPOTHE ILOAL PROTEIN NICKOZOT [H.sapiens]	ESTs	ESTs	EST	ESTs, Weakly similar to F25H5.6 [C.elegans]	ESTs	ESTs	Rattus norvegicus brain-enriched SH3-	domain protein mRNA, complete cds	ESTs	Rattus norvegicus pEachy mRNA,	complete cds	ESTs, Weakly similar to AF165892_1	RNA-binding protein SiahBP	[R.norvegicus]	ESTs	EST	ESTs	ESTs	EST	EST	ESTs, Highly similar to myosin X	[M.musculus]	Actin-related protein complex 1b	ESTs
	Known Gene Name																										Actin-related protein complex 1b	
	GenBank Acc ID3			967	538	784	342	336	194	358		1921	226		066			514	950	521	774	925	195	253		988	19289	756
		840 AI169041		676 AI071967	669 AI071538	1044 AI178784	671 AI071642	988 A1176836	788 AI112194	672 AI071858		124 AA849767	710 AI101226		677 AI071990			678 AI072014	228 AA891950	618 Al044621	221 AA891774	620 AI044925	622 AI045195	623 AI045253		816 AI137988	1673 NM_019289	1043 AI178756
	Nucleotide n Sequence In					F												_								~	1(1
-	GLGC Comparison	A		7				» E	1,1				O		0			~	A,M	4	4,G	3	\ \ \	>		~	 !:	
TABLE 1	SEGC	9627		9635 N	9668 K	9674	9697 K	Q712 R F	9754 A	9766 R		9775	9784 (9296 C			9800 R	9826 A,M	9889 A	9905 A,G	9925 S	3969 K	M 7766		10002 K	10016 F,	10019

D9917800.073404

Document Number 1650775		Unigene Cluster Title	EST	Ribosomal protein S5	Rattus norvegicus E-septin long form	mRNA, complete cds	ESTs	ESTs	ESTs	Inhibitor of DNA binding 1, helix-loop- helix protein (splice variation)	Rattus norvegicus SERP1 mRNA, complete cds	CCT. Moderately similar to	CO5_HUMAN COMPLEMENT C5	PRECURSOR [H.sapiens]	ESTs		R.norvegicus gene for glycogen	phosphorylase (liver type)	ESTs, Highly similar to HG17_RAT	NONHISTONE CHROMOSOMAL	PROTEIN HMG-1/ [K.norvegicus]	EST	Rattus norvegicus outer mitochondrial	membrane receptor r I OMZU mKNA,	contiblete cos	Rattus norvegicus outer mitochondriai	memoralie leceptor i conzo ilivia,	complete cus	ESTS
		Known Gene Name		Ribosomal protein S5						Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)				Complement component 5		HHs:phosphorylase, glycogen; liver	(Hers disease, glycogen storage	disease type VI)											
		Pathways															Starch and sucrose	metabolism		-									
Hillian Commission of the Comm	GenBank	AccID	639 AI058746	1502 X58465		102 AA819530	1363 H33426	985 AI176781	644 AI059444	1574 NM 012797	007.4	506 AF 100470		1205 AI233300	337 AA943564			1696 NM 022268			635 AI058430	269 AA894027			1341 D63411			1455 U21871	39 AA801255
	Nucleotide	800 (MA)	639	1502		102	1363	985	644	1574		onc		1205	337			1696			635	269			1341			1455	39
TABLE 4	Comparison		۳	10109 A		10176 A	10184 F		10200 L	40048 A	V 04-70	10306		10378 F	10394 R			10509 A			10533 S	10540 0			10544 A,B			10545 A	10549 C,D,E

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Document Number 1650775			Unigene Cluster Title	ESTs	ESTs, Highly similar to EST00098	protein [H.sapiens]	ESTs	Rattus norvegicus RNA-binding protein	SiahBP mRNA, partial cds	EST	ESTs	ESTs, Weakly similar to HP33	[R.norvegicus]	ESTs	Dotter propositive cteroid sensitive dene	A profession (SSG-1) mRNA complete cids	I protein (556-1) miner, complete cus	EST, Moderately similar to Ar U99 180_1	EH domain-containing protein EHD1	[M.musculus]	ESTs, Highly similar to	phosphatidylserine synthase-2	[M.musculus]	EST					Glutamine synthetase (glutamate- ammonia ligase)
			Known Gene Name																										Glutamine synthetase (glutamate- ammonia ligase)
			Pathways																						Aminoacyl-tRNA	prosjinitesis, Alginine and proline metabolism.	Glutamate metabolism,	Nitrogen metabolism,	Porphyrin and chlorophyll metabolism
		Sequence GenBank	ID Acc ID	876 AI170673		704 AI100878	1018 AI177790		1273 AI236366	602 AI043728	687 AI072476		842 AI169156	106 AA819767			1705 NM_022543			668 AI071456			673 AI071867	674 AI071868					1629 NM 017073
		GLGC Comparison	r 200	α	2000	10594 F	10611		10667 N	10790 F.M	10879 A N		10984 A P	11021 A,N			11039 G			11048 F	1		11125	11127 E				4144	11152

					101
GLGC Comparison ID Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	The Prince of State of Title of the State
			Aminoacyl-tRNA		
			proline metabolism,		
			Glutamate metabolism,		
			Nitrogen metabolism,		
11153 G	1629 NN	1629 NM 017073	Porphyrin and chlorophyll metabolism	Glutamine synthetase (glutamate- ammonia ligase)	Glutamine synthetase (glutamate- ammonia ligase)
11157 A.E	1184 AI232494	232494			ESTs
					ESTs, Highly similar to KIAA0315
11166 A	40 AA	40 AA801346			[H.sapiens]
					ESTs, Weakly similar to TISB_RAT
11172 P	338 AA	338 AA943730			TIS11B PROTEIN [R.norvegicus]
11174 E	333 AA	333 AA942745			ESTs
11179 A,H	783 AI1	783 AI111559			ESTs
11205 A,G	919 AI172057	172057			ESTs
					ESTs, Moderately similar to weak
					similarity to Arabidopsis thaliana
11215 E	49 AA	49 AA817921			ubiquitin-like protein 8 [C.elegans]
11227 0	541 AI010660	010660			ESTs
11228 A	739 AI102871	102871			ESTs
					ESTs, Weakly similar to similar to
					C.elegans hypothetical protein
					CET01H8.1, CEC05C12.3, CEF54D1.5.
					similar to trp and trp-like proteins
11235 D	1068 AI179709	179709			[H.sapiens]
					ESTs, Moderately similar to hepatoma-
11280 R	808 AI	808 AI137420			derived growth factor [M.musculus]
					ESTs, Moderately similar to imogen 44
11315 R	892 A1171229	171229			[M.musculus]

Document Number 1650775	Unigene Cluster Ditte	ESTs, Highly similar to Unknown	[H.sapiens]	ESTs	ESTs	ESTs	ESTs					ESTs, Highly similar to SPEE_MOUSE	SPERMIDINE SYNTHASE [M.musculus]					ESTs, Highly similar to SPEE_MOUSE	SPERMIDINE SYNTHASE [M.musculus]	ESTs, Moderately similar to	PTN3_HUMAN PROTEIN TYROSINE	PHOSPHATASE, NON-RECEPTOR	TYPE 3 [H.sapiens]	ESTs, Moderately similar to	PTN3_HUMAN PROTEIN TYROSINE	PHOSPHATASE, NON-RECEPTOR	TYPE 3 [H.sapiens]
	Known Gene Name s												HMm:spermidine synthase						HMm:spermidine synthase								
	Pathways:							Arginine and proline	metabolism, Selenoamino	acid metabolism, Urea cycle	and metabolism of amino	groups,beta-Alanine	metabolism	Arginine and proline	metabolism, Selenoamino	acid metabolism, Urea cycle	and metabolism of amino	groups,beta-Alanine	metabolism								
	GenBank Acc ID		526 AI009492	828 AI145556	388 AA946441	833 AI146215	835 AI146237						889 AI171088						1291 AI237002				26 AA799812		•		26 AA799812
	GLGC Comparison Sequence		526	828	388	833	835						388 —						1291				26				26
	Comparisor	T I	Ш	O	R	R	A						11403 A,D,L						11404 A.C.D.L				Ø				11423 B,H,Q
TABLE	g วอาอ		11322 E	11331 C	11336 R	11354 R	11357 A						11403						11404				11422				11423

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Document Number 1650775		Unigene Gluster Title 💎 🔭	ESTs, Moderately similar to	PTN3_HUMAN PROTEIN TYROSINE	PHOSPHATASE, NON-RECEPTOR	TYPE 3 [H.sapiens]	ESTs	ESTs	ESTs, Moderately similar to	41BB_MOUSE 4-1BB LIGAND	RECEPTOR PRECURSOR	[M.musculus]	ESTs, Moderately similar to progression	elevated gene 3 protein	[R.norvegicus],Rattus norvegicus	progression elevated gene 3 protein	mRNA, complete cds	ESTs, Highly similar to nuclear	transcriptional repressor Mph1	[M.musculus]	ESTs	ESTs, Weakly similar to putative	serine/threonine protein kinase MAK-V	[M.musculus]	ESTs, Weakly similar to putative	serine/threonine protein kinase MAK-V	[M.musculus]	ESTs, Weakly similar to putative	serine/threonine protein kinase MAK-V	[M.musculus]	ESTs
		Known Gene Name																													
														-																	
	Sank	ID Pathways				05	90	68				84					918			48	45									01	52
	Nucleotide GenBank	ID Acc ID				896 AI171305	862 AI169706	922 AI172189		•		1263 AI236084					487 AF020618			1248 AI235348	770 AI105145			1356 H31287			1356 H31287			991 AI176901	906 A1171652
TABLE1	GLGC Comparison	ID Code				11426 H	11429 A,G	11438 E				11465 0					11483 J			11485 E	11492 A			11493 J			11494 J			11495 J	11504 A,B

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Document Number 1650775	Known Gene Name. Unigene Cluster Title	ESTS, Weakly similar to CAG6_RAT	1,4-GALACTOSIDE ALPHA-2,3-	SIALYLTRANSFERASE [R.norvegicus]	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs, Moderately similar to S65785 mel-	13a protein - mouse [M.musculus]	ESTs	ESTs	ESTs	ESTs, Highly similar to small EDRK-rich	factor 2 [M.musculus]	ESTs, Weakly similar to ARL5_RAT	ADP-RIBOSYLATION FACTOR-LIKE	PROTEIN 5 [R.norvegicus]	ESTs	ESTs	ESTs, Weakly similar to B39066 proline-	rich protein 15 - rat [R.norvegicus]	ESTs, Highly similar to AF167573 1	protein methyltransferase [M.musculus]	Rattus norvegicus mRNA for Sulfotransferase K2
THE CONTRACT OF THE CONTRACT O	Pathways																			-						
	GenBank Acc ID			443 AA997068	1108 AI229307	984 AI176739	1200 AI233182	728 AI102560	832 AI146177		78 AA818721	665 AI071194	172 AA859633	701 AI100769	-	930 AI172471			708 AI101167	173 AA859645	1247 AI235282		725 AI102093		1050 AI178944	327 AA926193
	Nucleotide Sequence ID			443	1108	984	1200	728	832		78/	99	172	701		930			1802	173	1247		725		1050	327
1	GLGC Comparison ID Code			∢	A,C,R	A	O	A	A		Ш	Σ	L			Ш			2	A,G	K,O		F,M		C,D	A,E
TABLE 1	OI CELGC			11520 A	11527 A,C,R	11536 A	11561 C	11563 A	11576 A		11590 E	11596 M	11608 F	11619		11623 E		-	11625 R	11635 A,G	11644 K,O		11645 F,M		11660 C.D	11691 A,E

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TABLE 1					Document Number 1650775
Gl GC Comparison	Nucleotide Sequence	GenBank			
ID Code		Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
					Rattus norvegicus mRNA for
11693 A,C,D,E,K	836	836 AI168953			Sulfotransferase K2
11700 E	557	557 AI012574			ESTs
					ESTs, Highly similar to RNA cyclase
11720 B,O,Q	1174	1174 AI232273			homolog [H.sapiens]
11724 K	736	736 AI102812			ESTs
11731 P	1544	1544 NM_012561		Follistatin	Follistatin
11742 A,E	713	713 AI101262			ESTs
				translocator of inner mitochondrial	translocator of inner mitochondrial
11745 A	475	475 AB006450		membrane 17 kDa, a	membrane 17 kDa, a
					ESTs, Weakly similar to DP1_MOUSE
					POLYPOSIS LOCUS PROTEIN 1
11821 0	653	653 AI070350			HOMOLOG [M.musculus]
11830 N	1052	1052 AI179093			ESTs
					Rattus norvegicus mRNA for
11840 N	1526	1526 Y15068			Hsp70/Hsp90 organizing protein
					R.norvegicus mRNA for ribosomal
11850 G	1431	1431 R46985			protein L10a
11876 L	522	522 AI009321			ESTs
11893 B	1139	1139 AI230951			ESTs
				Brain immunoglobulin like protein with	
				tyrosine - based activation	Brain immunoglobulin like protein with
				motifs, Protein tyrosine phosphatase,	tyrosine - based activation motifs, Protein
				non-receptor type substrate 1 (SHP	tyrosine phosphatase, non-receptor type
11904 B,F,M,Q	1344	1344 D85183		substrate 1)	substrate 1 (SHP substrate 1)
11940 F,H	209	209 AA891108			ESTs
11959 A	217	217 AA891735			ESTs

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Document Number 1650775		Unigene Cluster Title	ESTs, Weakly similar to EPOR_RAT	ERYTHROPOIETIN RECEPTOR	PRECURSOR [R.norvegicus]	ESTs			ESTs, Highly similar to K6PP_KA1 6-	PHOSPHOFRUCTOKINASE, TYPE C	[R.norvegicus]	ESTs	ribonuclease 4	ESTs		cytochrome P450, 2b19		cytochrome P450, 2b19		cytochrome P450, 2019		cytochrome P450, 2019	777	cytochrome P450, 2019	ESTs, Weakly similar to Cys2/His2 zinc	finger protein [R.norvegicus]	Rattus norvegicus replication factor C	subunit 2 (RFC2) mRNA, partial cds	ESTs, Weakly similar to translation	initiation factor [M.musculus]
		Known Gene Name								Hsp:6-PHOSPHOFRUCTOKINASE,	TYPEC		ribonuclease 4			cytochrome P450, 2b19														
		Pathways					Fructose and mannose	metabolism, Galactose	metabolism, Glycolysis /	Gluconeogenesis, Pentose	phosphate cycle				Fatty acid metabolism,	Tryptophan metabolism														
	GenBank	AccID			220 AA891740	363 AA944958					1393 L25387	32 AA800429	1683 NM 020082	121 AA849365		1370 J00728		1378 K00996		1379 K01721		1383 L00320		66 AA818412		890 AI171094		273 AA899195		274 AA899256
	Nucleotide Sequence	₽.			220	363					1393	32	1683	121		1370		1378		1379		1383		99		890		273		274
+	GLGC Comparison Sequence	Code			×	В					œ	A	A	0		¥		12156 B,G,K		¥		×		A,K		ц		<u>~</u>		
TABLE 1	2979	9			11960 K	11974 B					12058 R	12064	12087 A	121200		12155 K		12156		12157 K		12158 K		12160 A,K		12185 F	2	12198 R		12203

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Document Number 1650775		Known Gene Name Unigene Cluster Title	ESTs, Moderately similar to	monoglyceride lipase [M.musculus]	ESTs	ESTs	ESTs	ESTs	ESTs, Moderately similar to LECT2	precursor [H.sapiens]	ESIS	ESTs, Weakly similar to cytoplasmic	aminopeptidase P [R.norvegicus]	ESTs, Weakly similar to cytoplasmic	aminopeptidase P [R.norvegicus]	ESTs	ESTs, Highly similar to p116Rip	[M.musculus]	ESTs, Weakly similar to predicted using	Genefinder [C.elegans]	ESTs	ESTs	ESTs	ESTs	Rattus norvegicus cyclin H mRNA,	complete cds	ESTs, Highly similar to AF151803_1 CGI	45 protein [H.sapiens]	ESTs	ESTs, Highly similar to hypothetical protein [H.sapiens]
		Pathways																												
	GenBank			696 AI072959	1106 AI229240	342 AA943800	360 AA944898	263 AA893453	272 4 404 5506	AA943390	1237 A1234301	0040400	389 AA940400		389 AA946466	433 AA965031	414.00.470	798 AI1364 / 8	i.	755 AI103955	1191 AI232706	1193 AI232924	413 AA957433	1122 AI230056		779 AI111344		380 AA946034	1120 AI229979	1357 H31620
	Nucleotide 1 Sequence			969	1106	342	360	263	270	3/2	1237	COC	389	(388	433	1	86/	L	cc/	1191	1193	413	1122		779	(380	1120	1357
1	Comparison	Code	i	E,S	А	M,P	12306 A,E,N	A	Ç	G E D	۲,۵	<	Υ		A	0	_	<u>.</u>	(A,F	g	S	A			F,M	(0	A	
TABLE	2979	₽		12215 E,S	12216 A	12277 M,P	12306	12312 A	10211	12314 G	25	10001	15021 A	00007	12332	12361	10075	123/3	7	12450 A,P	12463 Q	12467 S	12471	12551		12577	i i	12585	12587	12613

C C C C C C C C C C C C C C C C C C C	Document Number 1650775		Acc ID Pathways Known Gene Name Unigene Cluster Title	3 A1175294 ESTs	8 AA998029 ESTs	6 AI233836 ESTs	6 AA957906 ESTs	ESTs, Weakly similar to LIS1_MOUSE	PLATELET-ACTIVATING FACTOR		S A IO 1800		LS1s, Weakly similar to hemomucin [D.melanogaster]		2 Al11558 ESTs	6 AA955564 ESTs	8 AI228291 ESTs	6 AI237580 ESTs	7 AI236227 ESTs	2 A112926 ESTs	4 AI112969 ESTs	6 A1176276 Aminosugars metabolism pyrophosphorylase 1 ESTs		ESTs, Highly similar to potential membrane protein C14orf1 [H sapiens]	ESTs, Highly similar to CBG_RAT	
Comparison Sequence Comparison Sequence Code D D D D D D D D D	Section (Section Control of Contr		Pathways													•						sugars metabolism				
Comparison Sequeration Sequera			AccID	AI175294	AA998029	AI233836	AA957906			A10400E0	AI011809	AI072054	AA892916	AI072866	AI111558	AA955564	AI228291	AI237580	AI236227	AI112926	AI112969	AI176276	AI136702	A1179100		
Code Comparison Code Code Code Code Code Code Code Code		Nucleotide Sequence	D	933	458	1226	416			533	548	629	251	694	782	396	1088	1296	1267	792	794	926	801	1054		
	TABLE1	GC Comparison	ID Code	12614 C,D,R	12625 R	12655 A,O	12694 A			71.70	746 0	344 N	12848 A,G	12857 N	12880 E	12928 B,F,R	12946 A,N	12956 L	12964 N	12965 C	12969 J	12999 C	13045 M	13055 F		_

Document Number 1650775		Unigene Cluster Little	ES IS, Weakly Similar to PPP5_KAI SERINE/THREONINE PROTEIN		ESTS, Weakly similar to PPP5_RAT		ESTs	ESTs	ESTs	ESTs	ESTs, Moderately similar to LZIP-1 and	LZIP-2 [M.musculus]	ESTs		Ornithine carbamovitransferase	ESTs. Weakly similar to TCPA RAT T-	COMPLEX PROTEIN 1, ALPHA	SUBUNIT [R.norvegicus]	ESTs	ESTs	ESTs	ESTs	Rattus norvegicus UDP-	glucose:ceramide glycosyltransferase	mRNA, complete cds	ESTs	ESTs
		Known Gene Name		HMm:FK506 binding protein 4 (59 kDa)		HMm:FK506 binding protein 4 (59 kDa)									Ornithine carbamovltransferase									HHs:UDP-glucose ceramide	glucosyltransferase		
		Pathways												Arginine and proline	metabolism, Urea cycle and metabolism of amino groups									Sphingoglycolipid	metabolism		
	GenBank	Acc ID		1158 AI231547		552 AI012177	1039 AI178736	965 AI176465	1096 AI228728	154 AA858760		1059 AI179264	719 AI101708		1598 NM 013078	20010-		1220 AI233731	257 AA893080	62 AA818271	938 AI175508	934 AI175338			817 AI138034	957 AI176284	382 AA946187
	Nucleotide n Sequence	۵		1158		552	1039	965	1096	154		1059	719		1598			1220	257	62	938	934			817	957	382
- u	්	Code		0		0	A.R	Ш	A,C	0		13251 C,D,R	J.					۵	B,Q	A,H	N,N	13458 C,D,I			0	2	ш
TABLE	2979	₽		13092		13093 B O	13166 A.R	13175 E	13203 A,C	13229 0		13251	13265		13283 4	1020		13294 D	13332 B,Q	13351 A,H	13353 M,N	13458			13467 C	13501 R	13534 E

Document Number 1650775			ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to S26812	transcription factor ATF-4 - mouse [M.musculus]	ESTs	ESTs, Highly similar to RL3_RAT 60S	KIBOSOMAL PROTEIN L3	anan aseatorn anina surina nuntasan	complete cds	ESTs.Rat alpha-crystallin B chain		ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to KIAA0859	protein [H.sapiens]	ESTs	ESTs	ESTs	ESTs
		Known Gene Name						, side = 1							Crystallin, alpha polypeptide 2												
7 . The		Pathways																									
	4-0-0	AccID	367 AA945090	28 AA800169	1030 AI178507	1035 AI178602		1061 AI179381	814 AI137761		760466	707 100	04 040770	01101044	1419 M55534	1089 AI228540	1094 AI228676	1129 AI230326	947 AI175871	1101 AI229167	1111 AI229416		1117 AI229832	1127 AI230270	569 AI013832	AA799601	1142 AI230988
		QI	367	28	1030	1035		1061	814		000	enc	ō	0	1419	1089	1094	1129	947	1101	1111		1117	1127	269	17	1142
		Code	B,E,L,N		 	ш		■ 4	E H		L	13040 C,U,E		A,D,I				A,E		R	R		C.D	M	Ш	I	E,H,N
TABLE		၁၂၅ ၂၅ ၂၅	13557 B,E,	13568 H	13580 K	13581		13634 A	13640 E.H		0	13040	0	13684 A,D,	13723 D	13749 A	13757 A	13762 A.E	13799	13812 R	13838 R		13874 C.D	13895 M	13918 E	13926 H	13932 E,H,N

Document Number 1650775	Unigene Cluster Title	ESTs, Moderately similar to SEC HUMAN SEC PROTEIN	[H.sapiens]	ESTs	EST	ESTs	ESTs	Rattus norvegicus SH3-containing protein p4015 mRNA, complete cds	Rattus norvegicus SH3-containing	protein p40 to linking, complete cas	1,2-dioxygenase [M.musculus]	ESTs, Weakly similar to PIR1	[H.sapiens]	ESTs, Highly similar to DDX6_MOUSE	PROBABLE ATP-DEPENDENT RNA	HELICASE P54 [M.musculus]	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to AF073727_1	EH domain-binding mitotic	phosphoprotein [H.sapiens]	ESTs	EST
	K Known Gene Name									1112. Same acceptant of a disconsistent of the second of t	(homogentisate oxidase)														
	F Pathways										Tyrosine metabolism							-							
	GenBank Acc ID		1149 AI231193	1154 AI231388	1155 AI231439	1281 AI236679	1166 AI231808	489 AF026505		211 AA891194	1177 AI23238		1183 AI232489			1243 AI235046	1206 AI233323	1198 AI233164	1009 AI177181	1211 AI233468			1199 AI233172	1207 AI233361	1208 AI233367
	Nucleotide n. Sequence ID		1149	1154	1155	1281	1166	489		211	1177		1183			1243	1206	1198	1009	1211			1199	1207	1208
E-1	GLGC Comparison		Ω.	3 A,O	E L	ğ	' A,E	Ш		<u> </u>	_ ₹		14051 A,C,D			<u></u> 田	Y 1	l P	3 A	5 A			<u>×</u>	3.8	3 A
TABLE	2979 2979		13949 R	13963 A,O	13967 E	13992 Q	14007 A,E	14016 F		14017	14035 A		14051			14053 E	14074 A	14081 P	14083 A	14095 A			14103 A	14116 S	14118 A

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Document Number 1650775	Unigene Cluster Title	Rattus norvegicus tropomyosin non- muscle isoform NM1 (TPM-gamma) mRNA, complete cds,Rattus norvegicus tropomyosin non-muscle isoform NM3 (TPM-gamma) mRNA, complete cds	EST, Highly similar to PPOX_MOUSE PROTOPORPHYRINOGEN OXIDASE [M.musculus],EST, Moderately similar to PPOX_HUMAN PROTOPORPHYRINOGEN OXIDASE [H.sapiens]	ESTs, Weakly similar to cDNA EST yk249b3.5 comes from this gene [C.elegans] ESTs	Rattus norvegicus guanine aminohydrolase (GAH) mRNA, complete cds	ESTS ESTs	ESTs ESTs, Moderately similar to TFG protein [M.musculus]	ESTs ESTs, Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
	Known Gene Name	HHs:neurotrophic tyrosine kinase, receptor, type 1	HMm:protoporphyrinogen oxidase		HMm:guanine deaminase			Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
	Pathways		Porphyrin and chlorophyll metabolism		Purine metabolism			Purine metabolism
	Nucleotide GenBank ID Acc ID	1062 A179415	175 AA859700	1024 AI178073 1233 AI234107	177 AA859837	775 AI105205 1234 AI234133 182 AA859994	723 AI102017 1140 AI230956	1086 Al228197 21 AA799729
TABLE1	omparison Code	14126 E	14139 H	14171 E 14181 A	14185 P	14199 K 14706 A	14208 A,B 14224 C	14242 C,D 14250 K

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Document Number 1650775	Page 1	Unigene Cluster Title	ESTs	ESTs, Weakly similar to bK126B4.2	[H.sapiens]	ESTs, Highly similar to phosphoprotein	[M.musculus]	ESTs, Highly similar to KIAA1049 protein	[H.sapiens]	ESTs, Moderately similar to UBE-1b	[M.musculus]	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs, Moderately similar to	mitochondrial DNA polymerase	accessory subunit [M.musculus]	ESTs	ESTs	ESTs	ESTs, Highly similar to gp250 precursor	[M.musculus]	ESTs	ESTs, Moderately similar to glutathione-	S-transferase homolog [M.musculus]
		Known Gene Name :																												
		Pathways															•													
	GenBank	Acc ID	1118 AI229902		1181 AI232409		1366 H33842		1148 AI231159		1261 AI236036	233 AA892146	1006 AI177115	171 AA859585	858 AI169620	654 AI070421	1235 AI234152	826 AI145095	703 AI100871			253 AA892950	535 AI010147	25 AA799804	1359 H32584		132 AA850618	793 AI112964		1250 AI235360
	Nucleotide Seguence		1118		1181		1366		1148		1261	233	1006	171	828	654	1235	826	703			253	535	25	1359		132	793		1250
1	GLGC Comparison	Code	S		S		0				A,E	۵	E	A	F,M	A,J	Ш	Ľ,	C,D			L	M	M,P	A		S	A,G		4
TABLE	9F GC	9	14258 (14264 S		14266		14303		14312 A,E	14330 P	14335	14353 A	14400 F,M	14424 A,J	14449 E	14458 C,	14462 C,D			14465	14491 M	14504 M,P	14506 A		14507 S	14512 A,G		14584 4

Document Number 1650775		ster litte				ilar to Nibrin	to ORF YKR081c			ilar to KIAA0922					to /prediction			o lipoic acid	[6			rague Dawley	ptor mRNA,		o integrase	norvegicus	ein kinase C	alata cde
Document		Unigene Cluster I Itle	ESTs	ESTs	ESTs	ESTs, Moderately similar to Nibrin IM.musculusl	ESTs, Weakly similar to ORF YKR081c	[S.cerevisiae]	ESTs	ESTs, Moderately similar to KIAA0922	protein [H.sapiens]	ESTs	ESTs	ESTs	ESTs, Weakly similar to /prediction	Esterase 2	ESTs	ESTs, Highly similar to lipoic acid	synthetase [H.sapiens]	ESTs	ESTs	Rattus norvegicus Sprague Dawley	protein kinase C receptor mRNA,	complete cds	ESTs, Highly similar to integrase	meración la procent [M musculus] Battus norvegicus	Sprague Dawley protein kinase C	rocenter mDNA complete cde
			Ш	Ш	Ш	Ш €	· W	5]	3	Ш	d		Ш	Ш,	Ш	Ш	ш.		S		ш	<u> </u>	<u>a</u>	3			2 0)	\$
		Known Gene Name														Esterase 2												
		Pathways														نن												
		Pa																										
	GenBank	Acc ID	232 AA892128	38 AA801076	1290 AI236989	803 01137040		1240 AI234830	997 AI176993		1252 AI235584	1256 AI235895	1258 AI235950	1301 AI237698	1264 AI236089	1324 D00362	1274 AI236461		1293 AI237159	1090 AI228557	105 AA819744			1444 U03390				1
	Nucleotide Sequence	ID	232	38	1290	803	200	1240	266		1252	1256	1258	1301	1264	1324	1274		1293	1090	105			1444				000
	omparison	Code		ĸ	Q,			C,D	0				,E,N				2		щ	Q,								(
TABLE 1	2 22 19	a	14595 S	14600 E,R	14619 C,D	1 1620	1	14693 A,C,D	14738 N.O		14746 A	14767 A	14776 A,E,N	14840 K	14869 A	14882 S	14913 L.		14937 A,E	14939 C,D	14958 N			14959				

Document Number 1650775		Unigene Cluster Title	ESTs, Highly similar to ENHANCER OF	RUDIMENTARY HOMOLOG	[M.musculus]	Rattus norvegicus sulfite oxidase mRNA,	complete cds	Integrin, beta 1	Tissue-nonspecific ALP alkaline	phosphatase	Tissue-nonspecific ALP alkaline	phosphatase	Rattus norvegicus tissue inhibitor of	metalloproteinase-1 (TIMP1), mRNA,	complete cds	Rattus norvegicus tissue inhibitor of	metalloproteinase-1 (TIMP1), mRNA,	complete cds	Rattus norvegicus tissue inhibitor of	metalloproteinase-1 (TIMP1), mRNA,	complete cds	ESTs	ESTs	ESTs	ESTs, Weakly similar to development-	related protein [R.norvegicus]	ESTs	Methylacyl-CoA racemase alpha	ESTs, Highly similar to ATDA_MOUSE	DIAMINE ACETYLTRANSFERASE	
		Known Gene Name					HHs:sulfite oxidase	Integrin, beta 1	Tissue-nonspecific ALP alkaline	phosphatase	Tissue-nonspecific ALP alkaline	phosphatase																Methylacyl-CoA racemase alpha	Spermidine / spermine N1-	acyltransferase (diamine	
		Pathways					Sulfur metabolism		Folate biosynthesis,	Glycerolipid metabolism	Folate biosynthesis,	Glycerolipid metabolism																		Arginine and proline	
	de GenBank				845 AI169171		218 AA891738	1012 AI177366		1597 NM_013059		1597 NM_013059			851 AI169327			851 AI169327			1244 AI235224	961 AI176363	925 AI172285	430 AA964688		878 AI170696	113 AA848378	1576 NM_012816			
	Nucleotide	Ω.			& —		2	10		15.					œ			α			12.	Õ	6	4			1	15			-
TABLE 1	GLGC Comparison	D C30			14962 A,C,D		14970 G	14989 O		14996 A,N		14997 A,E,N,O			15002 F			15003 F			15004 A	15015 S	15016 A	15018 E,S		15029 A,C,D,E,P	15030 L	15032 A,D			

TARIE 1				Document Number 1650775
	Nucleotide			
GLGC Comparison	Sequence GenBank	k Pathways	Known Gene Name	Unigene Cluster Title
			HHs:cytochrome P450, subfamily IID	
		Fatty acid metabolism,	(debrisoquine, sparteine, etc., -	Rattus norvegicus cytochrome P450
15055 A	1463 U48220	Tryptophan metabolism	metabolizing), polypeptide 6	2D18 mRNA, complete cds
15057 0	1675 NM_019291	11 Nitrogen metabolism	carbonic anhydrase 2	carbonic anhydrase 2
			HHs:farnesyl diphosphate synthase	
			(farnesyl pyrophosphate synthetase,	Rat testis-specific farnesyl
			dimethylallyltranstransferase,	pyrophosphate synthetase mRNA,
15070 H	1081 AI180442	Sterol biosynthesis	geranyltranstransferase)	complete cds
				ESTs, Highly similar to OS-4 protein
15080 A	724 AI102045			[H.sapiens]
15089 F	530 AI009752			ESTs
15091 J	1040 AI178740		YY1 transcription factor	ESTs
			Insulin-like growth factor-binding protein	Insulin-like growth factor-binding protein Insulin-like growth factor-binding protein
15097 L,O	1548 NM 012588	82	(IGF-BP3)	(IGF-BP3)
				ESTs, Highly similar to dJ1118D24.1c
15113 A,G	941 AI175590			[H.sapiens]
				ESTs, Highly similar to sorting nexin 4
15116 P	190 AA874928			[H.sapiens]
				Rattus norvegicus interferon-inducible
15121 E	746 AI103159	٠		protein 16 mRNA, complete cds
				ESTs, Weakly similar to Sid1669p
15122 E	1176 AI232303			[M.musculus]
		Androgen and estrogen		Rattus norvegicus UDP-
		metabolism,Pentose and		glucuronosyltransferase (UGT1.1) gene,
		glucuronate		complete cds,Rattus norvegicus UDP-
		interconversions, Porphyrin		glucuronosyltransferase UGT1A7
		and chlorophyll		mRNA, complete cds,UDP-
		metabolism, Starch and	UDP-glucuronosyltransferase 1 family, glucuronosyltransferase 1 family,	glucuronosyltransferase 1 family,
15127 B,K	1434 S56937	sucrose metabolism	member 1	member 1

GenBank Acc ID Pathways 1021 144585 144585 M_017278 M_017278 A859327 A859341 A859362 237618 237792 237792 237792 237792 237792 237794 11794		
GLGC Comparison Nuclectide ID Code ID 15135 A,D 1436 S7 15136 A 20 AA 15139 H 818 AI 15141 E,F 1649 NN 15149 R 165 AA 15162 L 168 AA 15170 A,H,N 1299 AI 15171 J 169 AA 15172 H 1399 MI 15181 H 1245 AI 15190 N 729 AI 15191 N 964 AI 15197 A 778 AI	35 A,D 1436 S71021 36 A 20 AA799672 39 H 818 Al144585 41 E,F 1649 NM_017278 49 R 1648 AA859327 50 A,E 165 AA859341 50 L 168 AA859350 70 A,H,N 1299 Al237618 71 J 1160 Al231792 72 J 169 AA859362 72 J 169 AA859362 8 Al176675 1245 Al235234 30 M,N 1399 M11794 30 N 729 Al102562 31 N 964 Al176456 37 A 778 Al105444	15207 A,B,Q 1440 NM 046080

Document Number 1650775		Pathways Known Gene Name Unigene Cluster Title	activator CIDE-B [M.musculus]	ESTs, Highly similar to CSK_RAT	TYROSINE-PROTEIN KINASE CSK	[R.norvegicus]	ESTs	ESTs	ESTs	I polyphosphate histidine	phosphatase 1 phosphatase 1	multiple inositol polyphosphate histidine multiple inositol polyphosphate histidine	phosphatase 1	FK506-binding protein 1 (12kD) FK506-binding protein 1 (12kD)	B-cell translocation gene 2, anti-	proliferative	B-cell translocation gene 2, anti-		B-cell translocation gene 2, anti-	proliferative	ESTs	ESTs	calpactin I heavy chain calpactin I heavy chain	ESTs	cofilin 1, non-muscle cofilin 1, non-muscle	ESTS, Highly similar to IF39_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBLINIT 9	
	Jungan	Acc ID	609 AI044241			1011 AI177363	1328 D13623	1034 AI178573	148 AA858548		780 AI111401		484 AF012714	1602 NM_013102		1647 NM_017259		1647 NM_017259		1647 NM_017259	198 AA875126	198 AA875126	1021 AI177911	902 AI171587	1637 NM 017147		
	Si consumerations	Q	609			1011	1328	1034	148		780		484	1602		1647		1647		1647	198	198	1021	905	1637		
-		Code Companison	4			E,L		D,I,L	D				,	0		V		A,F		A	15312 C,D,I,J	C,D,J	0		٥		
TARIE	2) 	15240 A			15251 E,I	15281	15282	15283 D		15291		15292	15295 0		15299 A		15300 A,F		15301 A	15312	15313 C,D,J	15315	15345 L	15365 D		

Document Number 1650775		Unigene Cluster Title 🔯 🕆	ESTs, Moderately similar to ornithine	decarboxylase antizyme 2 [M.musculus]	ESTs	R.norvegicus mRNA for collagen alpha1	type I	ESTs	ATP citrate lyase	Microvascular endothelial differentiation Microvascular endothelial differentiation	gene 1	ESTs	Glucocorticoid receptor	R.norvegicus mRNA for histone H3.3	R.norvegicus mRNA for histone H3.3	Rattus norvegicus RNA polymerase I	127 kDa subunit mRNA, complete cds	ESTs	Rattus norvegicus mRNA for Tctex-1,	complete cds	Rat mRNA for 5E5 antigen, complete	cds	Rat mRNA for 5E5 antigen, complete	cds	Rattus norvegicus mRNA for multidrug	resistance-associated protein (MRP)-like	protein-1 (MLP-1), complete cds	Rattus norvegicus mRNA for multidrug	resistance-associated protein (MRP)-like	protein-2 (MLP-2), complete cds
		Known Gene Name					procollagen, type I, alpha 1		ATP citrate lyase	Microvascular endothelial differentiation	gene 1		Glucocorticoid receptor			HMm:RNA polymerase 1-2 (128 kDa	subunit)													
		Pathways							Citrate cycle (TCA cycle)							Purine metabolism,	Pyrimidine metabolism													
	GenBank	Acc ID		1138 AI230759	204 AA875537		1413 M27207	356 AA944401	1618 NM_016987		562 NM_012699	205 AA875620	1546 NM_012576	1016 AI177503	879 AI170709		488 AF025424	733 AI102739		940 AI175566		281 AA900009		921 AI172107			479 AB010466			1645 NM_017220
	Nucleotide Sequence	a		1138	204		1413	356	1618		1562	205	1546	1016	879		488	733		940		281		921			479			1645
	Comparison	Code		~	ſ		ග	B,N	A		7	ſ	I	A	エ		A,J	1,L		D,R		S		ŋ			A,D			F,G
TABLE	29 T9	Ω		15551	15558 J		15571	15606 B,N	15612 A		15616 J	15617	15634	15642	15645 K		15647 A,J	15655		15663 D,R		15672 S		15673			15700 A,D			15701 F,G

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Document Number 1650775		Unigene Cluster Title 1 K	Rattus norvegicus neutral solute channel	aquaporin 9 (AQP9) mRNA, complete	cds	Rattus norvegicus brain-enriched	guanylate kinase-associated protein 1	mRNA, complete cds	ESTs	ESTs, Moderately similar to NADH- 2 ubiquinone oxidoreductase B14.5B	subunit [H.sapiens]	ESTs, Weakly similar to phosphoserine	aminotransferase [H.sapiens]	ESTs, Weakly similar to phosphoserine	aminotransferase [H.sapiens]	ESTs, Weakly similar to phosphoserine	aminotransferase [H.sapiens]	ESTs	Rat guanine nucleotide-binding protein G	i, alpha subunit mRNA, complete cds	ESTs	ESTs	ESTs	R.norvegicus ARL1 mRNA for ARF-like	protein 1	ESTs
		Known Gene Name								HHs:NADH dehydrogenase ESTs, Moderately similar to NADH- (ubiquinone) 1, subcomplex unknown, 2 ubiquinone oxidoreductase B14.5B	(14.5kD, B14.5b)															
		Pathways								n,	Ubiquinone biosynthesis							ı								
		AccID			1718 NM_022960			1726 NM 024163	575 AI013924		286 AA900580		738 AI102868		738 AI102868		1126 AI230228	85 AA866276		99 AA875225	1074 AI179988	1202 AI233262	451 AA997711		200 AA875253	1175 AI232294
	Nucleotide Segrence				1718			1726	575		286		738		738		1126	185		199	1074	1202	451	,	200	1175
E 1	Comparisor	ID Code			A.K			<u>ш</u>	B,Q		B,E		О		C,D		15862 A,C,D	A,Q		조	AF	15900 A,C,D	LL.		A .	A,K,L
TABLE	2010	} -			15755 A,K			15778	15786 B,Q		15834 B,E		15860		15861		15862	15884 A,Q		15888 K	15892 A,F	15900	15914		15933 A	15955 A,K,I

Document Number 1650775		Unigene Cluster Title	ESTs	ESTs	ESTs	EST	Rattus norvegicus nucleosome assembly protein mRNA, complete cds	ESTs, Highly similar to NAD(P)+ transhydrogenase [M.musculus]	ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]	Herne oxygenase	Heme oxygenase	ESTs	ESTs	ESTs, Weakly similar to melanocyte- specific gene 1 protein [R.norvegicus]	Rattus norvegicus lin-7-Ba mRNA, complete cds	Rattus norvegicus clone BB.1.4.1 unknown Glu-Pro dipeptide repeat protein mRNA, complete cds	ESTs, Moderately similar to adipophilin
		Known Gene Name								Heme oxygenase							
		Pathways						Nicotinate and nicotinamide transhydrogenase (NAD(P)+metabolism transhydrogenase)		Porphyrin and chlorophyll metabolism	Porphyrin and chlorophyll metabolism						
	GenBank	AccID	972 AI176540	550 AI012130	186 AA866426	187 AA866435	497 AF062594	225 AA891872	1091 AI228596	1547 NM_012580	1067 AI179610	189 AA874889	1145 AI231011	994 AI176963	503 AF090134	265 AA893485	
	Nucleotide Seguence	Q	972	220	186	187	497	225	1091	1547	1067	189	1145	994	203	265	
-	GLGC Comparison	Code	E,L	Ь	エ	X	A,F	9		A,J,Q	Α,J,Ω	A,C,D		¥	G	Ι	
TABLE 1	25.EGC	9	15959	15961 P	15980 H	15987 K	16006 A,F	16023 G	16053	16080 A,J,Q	16081 A,J,Q	16085	16087	16124 K	16125 Q	16134 A,H	

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Document Number 1650775		Unigene Cluster Title	ESTs, Moderately similar to adipophilin	[H.sapiens]	ESTs, Weakly similar to C13B9.2	[C.elegans]	Rattus norvegicus intercellular calcium-	binding protein (MRP8) mRNA, complete	spo	ESTs, Weakly similar to ECHM_RAT	ENOYL-COA HYDRATASE,	MITOCHONDRIAL PRECURSOR	[R.norvegicus]	Rat mRNA for ribosomal protein S8	ESTs, Moderately similar to	AF133910_1 ARL-6 interacting protein-3	[M.musculus]	Secreted acidic cystein-rich glycoprotein	(osteonectin)	ESTs, Moderately similar to DHB2_RAT	ESTRADIOL 17 BETA-	DEHYDROGENASE 2 [R.norvegicus]	Rat brain glucose-transporter protein	mRNA, complete cds		R.norvegicus CYP3 mRNA	solute carrier family 12, member 4	ESTs	ESTs	ESTs, Moderately similar to
	2 P T)	Known Gene Name		<u>]</u>								_					1	ų	glycoprotein (osteonectin)				Solute carrier family 2 a 1 (facilitated	glucose transporter) brain		Hsp:CYTOCHROME P450 3A18	solute carrier family 12, member 4			
		Pathways																							acid metabolism,	Tryptophan metabolism				
	GenBank	Acc ID		598 AI030932		1179 AI232341			408 AA957003				757 AI104482	488 X06423			192 AA874999		1557 NM_012656			166 AA859342		347 AA944077		1338 D38381	1667 NM_019229	193 AA875032	167 AA859348	
	Nucleotide Sequence			598		1179			408				757	1488			192		1557			166		347		1338	1667	193	167	
-	G Comparison	Code		ш		⋖			M,P				A,S	_			I		9			M		E,Q		E,K	0	А	A	
TABLE	25.16	Q		16169 E		16172 A		******	16173 M,P				16190 A,S	16205			16215 H		16219 G			16240 M		16251		16278 E,K	16283 0	16312 A	16314 A	

Document Number 1650775	Unigene Cluster Title	ESTs, Weakly similar to DnaJ homolog 2	[R.norvegicus]	ESTs, Highly similar to TCPZ_MOUSE T	COMPLEX PROTEIN 1, ZETA	SUBUNIT [M.musculus]	ESTs		ESTs	ESTs, Weakly similar to	choline/ethanolamine kinase	[R.norvegicus]	Rattus norvegicus clone A-2 arylamine N	acetyltransferase mRNA, complete cds	R.norvegicus mRNA for V1a arginine	vasopressin receptor	L	L	ESTs	ESTs	ESTs, Highly similar to SMD2_HUMAN	SMALL NUCLEAR	RIBONUCLEOPROTEIN SM D2	[H.sapiens]	ESTs	farnesyl diphosphate farnesyl	transferase 1	ESTs
	Known Gene Name		[R.	ES	00	ns sn	ES	EST	ES	ES	cho	[R	Hsp:ARYLAMINE N-	ACETYLTRANSFERASE 1 ace	R.r	vas	EST	EST	ES	ES	S3	NS S	RII	H)	ES	farnesyl diphosphate farnesyl far	transferase 1 tra	ES
	Pathways												,,,														Sterol biosynthesis	
	GenBank Acc ID		174 AA859648			195 AA875047	1157 AI231506	184 AA866240	722 AI102009			196 AA875050		1442 U01344		235 AA892251	250 AA892888	250 AA892888	145 AA852027	145 AA852027				958 AI176294	214 AA891423		1669 NM_019238	362 AA944956
	Nucleotide Sequence ID		174			195	1157	184	722 ,			196		1442		235	250	250	145	145				928	214		1669	362
·	GLGC Comparison	<u> </u>				~	0	0	4			9,0				7,H	6	۵		0					4		+	3,0
TABLE	25.15 25.15		16318			16319 K	16321 C	16323 S	·16324 A			16327 A,O		16361 H		16364 A,H	16366 P	16367 F	16408 F	16409 S				16438	16446 A		16449 H	16458 B,Q

	7				Document Number 1650775
GLGC Comparison	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
I -	080	000			Rat low molecular weight fatty acid
1	2006	1000			ESTs. Moderately similar to hypothetical
	118	118 AA848782			protein [M.musculus]
I					ESTs, Weakly similar to HS9B_RAT HEAT SHOCK PROTEIN HSP 90-BETA
	973	973 AI176546			[R.norvegicus]
1	1530	1530 NM 042532	Porphyrin and chlorophyll	Openionio (formaldago)	Corntonlasmin (farrovidaso)
T	1362	T			ESTs
					Rattus norvegicus p38 mitogen activated
	904	904 AI171630			protein kinase mRNA, complete cds
					Rattus norvegicus mRNA for TIP120,
	1131	1131 AI230395			complete cds
					Rattus norvegicus muscle Y-box protein
	1333	1333 D2855/			YB2 mKNA, complete cds
	1230	1230 AI234079			ESTs
	837	837 AI168967			ESTs
	1150	1150 AI231196			ESTs
	1606	1606 NM_013132		Annexin V	Annexin V
	1606	1606 NM_013132		Annexin V	Annexin V
					R.norvegicus mRNA for macrophage
	1522	1522 X98517			metalloelastase (MME)
	759	759 AI104608			ESTs
	436	436 AA965190			ESTs

TOTAL COMPANIES

Document Number 1650775	Unigene Cluster Title	han Tyrosine 3-monooxygenase/tryptophan 7, 5-monooxygenase activation protein, eta polypeptide	Tyrosine 3-monooxygenase/tryptophan Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	ESTs	ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]	ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]	ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]	ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]	Rat ketohexokinase mRNA, complete cds	ESTs
	Known Gene Name	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Tyrosine 3-monooxygenase/tryptophs 5-monooxygenase activation protein, eta polypeptide						H _{SD} :KETOHEXOKINASE	
And the second s	Pathways								Fructose and mannose metabolism	
	GenBank Acc (D.	1596 NM_013052	1596 NM_013052	870 AI170327	517 AI008838	517 AI008838	1060 A1179300	AA686132	1427 M86235	1020 AI177885
	Nucleotide Sequence ID	1596	1596	870	517	517	1060	4	1427	1020
1	GLGC Comparison	_	0'1		16700 A,E,S	Ą	16703 A.C,O	တ	_ ∢	I
TABLE	GLGC DD	16683	16684	16688	16700	16701 A	16703	16704 S	16726 A	16728 H

DSG17888 OFS18

Document Number 1650775	Unigene Cluster Title :	ESTs, Moderately similar to	JIVI_HOMAN_JIV-I PROTEIN [H.sapiens]	ESTs	ESTs, Highly similar to glycyl-tRNA synthetase [H.sapiens]	ESTs	ESTs		ESTs, Highly similar to glutathione transferase [R.norvegicus]	ESTs, Weakly similar to nonmuscle myosin heavy chain-A [R.norvegicus]		ESTs	Rat alpha-2(I) promoter	- LCL
	Known Gene Name							Butanoate metabolism, Fatty acid biosynthesis (path 2), Lysine degradation, Tryptophan metabolism, Valine, leucine and Alanine metabolism Subunit Butatase (trifunctional protein), alpha			HSp:PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 2			
	Pathways							Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism						
Miles of the second sec	GenBank Acc ID		23 AA799766	336 AA943131	52 AA818089	632 AI058319	682 AI072137	D16478	1510 X62660	553 AI012215	1503 X58828	245 AA892602	188 AA866454	1083 A1036753
	Nucleotide Sequence ID		23	336	52	632	682	1331	1510	553	1503	245	188	1283
-	GLGC Comparison ID Code		Ą.		c,D	A	٨	7	щ Ж	0,1	3.0.0	1		NOW
TABLE	9 GC		16730 A,	16747	16756 C,D	16765 A	16766 A	16768 N	16780 E,K	16783 L,O	16809 B.O.O	16825 J	16854	16850 A C N

775																				•										
Document Number 1650775	E .	Unigene Cluster Title	Thymopoietin (lamina associated	polypeptide 2)	ESTs	ESTs, Weakly similar to nitrilase homolog 1 [M.musculus]									Rattus norvegicus 4-	trimethylaminobutyraldehyde	dehydrogenase (Tmabadh) mRNA,	complete cds									Rattus norvegicus 4-	trimethylaminobutyraldehyde	dehydrogenase (Tmabadh) mRNA,	complete cds
		Known Gene Name	Thymopoietin (lamina associated	polypeptide 2)												HHs:aldehyde dehydrogenase 9	(gamma-aminobutyraldehyde	dehydrogenase, E3 isozyme)										HHs:aldehyde dehydrogenase 9	(gamma-aminobutyraldehyde	dehydrogenase, E3 isozyme)
		Pathways					Arginine and proline	metabolism, Ascorbate and	aldarate metabolism, Bile	acid biosynthesis, Butanoate	metabolism, Fatty acid	metabolism, Glycerolipid	metabolism, Histidine	metabolism, Lysine	degradation, Propanoate	metabolism, Pyruvate	metabolism, Tryptophan	metabolism	Arginine and proline	metabolism, Ascorbate and	aldarate metabolism, Bile	acid biosynthesis, Butanoate	metabolism, Fatty acid	metabolism, Glycerolipid	metabolism, Histidine	metabolism, Lysine	degradation, Propanoate	metabolism, Pyruvate	metabolism, Tryptophan	metabolism
	otide ence GenBank			1583 NM_012887	848 AI169284	446 AA997345												754 AI103758								-				773 AI105188
	SLGC Comparison Sequence			-	1,E,F	J,C,D,I				-								B,E												,B,E,Q
TABLE 1	0979	9		16871 H	16879 A,E,F	16883 A,C,D,												16884 B						-						16885 A,B,E,Q

Acc ID Pathways AA925541 AA925541 AA925541 Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups AA819021 AI179236 NM 013144 AA799560 Galactose metabolism, Mucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism AI170679 Nostaglandin and No 019170 Ieukotriene metabolism	TABLE 1					Document Number 1650775
S 320 AA925541 S 320 AA925541 S 320 AA925541 Arginine and proline metabolism. Glycine, serine and threonine metabolism of amino groups G 92 AA819021 A 1608 NM 013144 A 1600 NM 019170 Beukotriene metabolism	GC Comparison D: Code			, Pathways	Known Gene Name	Unigene Gluster Title
S 320 AA925541 S 320 AA925541 S 320 AA925541 S 320 AA925541 Arginine and proline metabolism, Glycine, serine and threonine metabolism of amino groups A 1572 NM_012793 metabolism of amino groups A 1608 NM_013144 A 14 AA799560 Galactose metabolism, Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism A 929 A172417 Prostaglandin and Proline metabolism A POSTA A170679 sucrose metabolism Prostaglandin and Proline metabolism						ESTs, Moderately similar to
S 320 AA925541 S 320 AA925541 Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and threonine metabolism of amino groups G 92 AA819021 A 1608 NIM_013144 A 1608 NIM_013144 A 14 AA799560 Galactose metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism A 929 A1172417 Prostaglandin and feuropian metabolism	894 0	144	AA852018			AF097362_1 gamma-interferon inducible lysosomal thiol reductase IH.sapiens1
S 320 AA925541 Arginine and proline metabolism, Glycine, serine and threonine metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism, Urea cycle and metabolism of amino groups G 92 AA819021 A 1608 NM_013144 A 14 AA799560 Galactose metabolism, Nucleotide sugars metabolism, Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism A 929 A172417 Prostaglandin and leukotriene metabolism	944 S	320	AA925541			ESTs, Highly similar to protein L
A 1608 NM 013144 B 1600 NM 019170 leukotriene metabolism	3945 S	320	AA925541			ESTs, Highly similar to protein L IM.musculus]
Metabolism, Glycine, serine and threonine and threonine metabolism, Urea cycle and 1572 NM_012793 metabolism of amino groups G				Arginine and proline		
E				metabolism, Glycine, serine and threonine		
G 92 AA819021 1058 AI179236 1608 NM 013144	947 E	1572	NM 012793	metabolism, Urea cycle and metabolism of amino groups	Guanidinoacetate methyltransferase	Guanidinoacetate methyltransferase
P 1058 AI179236 A 14 AA799560 Galactose metabolism, Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism A,E 877 AI170679 sucrose metabolism A 929 AI172417 Prostaglandin and leukotriene metabolism	958 G	92	AA819021			EST
A 1608 NM 013144 A 799560 Galactose metabolism, Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and A,E 877 Al170679 sucrose metabolism A 929 Al172417 Prostaglandin and 1660 NM 019170 leukotriene metabolism	961 P	1058	AI179236			ESTs
A,E 877 AI170679 A 929 AI172417	982 A	1608	NM 013144		Insulin-like growth factor binding protein	Insulin-like growth factor binding protein Insulin-like growth factor binding protein
A,E 877 A1170679 A 929 A1172417	993 A	14	AA799560			ESTs
A,E 877 A1170679 A 929 A1172417				Galactose metabolism,		
A,E 877 A1170679 A 929 A1172417				Nucleotide sugars metabolism, Pentose and		ESTS. Highly similar to UDP1 HUMAN
A,E 877 A1170679 A 929 A1172417				glucuronate		UTPGLUCOSE-1-PHOSPHATE
A 929 AI172417 Prostaglandin and 1660 NM 019170 leukotriene metabolism	327 A,E	877	A1170679	interconversions, Starch and sucrose metabolism	HHs:UDP-glucose pyrophosphorylase	URIDYLYLTRANSFERASE 1
Prostaglandin and 1660 NM 019170 leukotriene metabolism	A 94	926	A1172417			ESTs, Weakly similar to Similarity to
l loon IVI of all leukotriene metabolism	- 100	0007	\top	iglandin and		Descrition of the property (Congrans)
	104 1	0991		riene metabolism	carbonyl reductase	carbonyl reductase

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Bocument Number 1650775		ne Unigene Cluster Title	Rattus norvegicus glutathione reductase	mRNA, complete cds	Rattus norvegicus glutathione reductase	mRNA, complete cds	Rattus norvegicus glutathione reductase	mRNA, complete cds	ribosomal protein S6	ESTs, Weakly similar to AC007080_2	NG38 [M.musculus]	Rat clathrin light chain (LCB2) mRNA,	complete cds, Rat clathrin light chain	(LCB3) mRNA, complete cds	ESTs, Highly similar to AF168795_1	schlafen-4 [R.norvegicus]	Rat mRNA encoding alpha-tubulin	ESTs	R.norvegicus ASI mRNA for mammalian	equivalent of bacterial large ribosomal	subunit protein L22	ESTs, Highly similar to eIF3 p66	[M.musculus]	ESTs, Weakly similar to p60 protein	[R.norvegicus]	Cyclin D3	Cyclin D3	Cyclin D3	Rattus norvegicus glycine-, glutamate-,	Ithienvicyclohexylpiperidine-binding
		Known Gene Name		HHs:glutathione reductase		HHs:glutathione reductase		HHs:glutathione reductase	ribosomal protein S6																	Cyclin D3	Cyclin D3	Cyclin D3		
	ار در این این این این	Pathways		Glutathione metabolism	Glutamate metabolism,	Glutathione metabolism	Glutamate metabolism,	Glutathione metabolism																						
	e GenBank			1474 U73174		1474 U73174			1638 NM_017160	1	1085 AI228042			1407 M15883		326 AA926129	699 NM_022298	566 AI013690			1501 X58389	7	Z 13 AA69 1333		219 AA891739	1568 NM_012766	1568 NM_012766	1568 NM_012766		
		Q.		147		147		25	163		108:			140		32(169	56		1	150		717		21(156	1568	1568		
E1	C Comparison	Code		17090 G,K		17091 G,K		Z X	7 E		7 K			4 A		7	8 H	7 M			5 A		-,-		6 A	17257 E,R	8 P	<u>т</u>		
TABLE	STO	9		1709		1709		17092 K	17107 E		17117 K			17154 A		17157	17158 H	17167 M			17175 A	47005	77/		17256 A	1725	17258 P	17261		_

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TABLE 1						Document Number 1650775
(E)	omparison	Nucleotide Sequence	GanBank		-1	
}	iidii inaaa	a	AccID	Pathways	Known Gene Name	Unigene Cluster Title
17281 M.P	M.P	1450	1450 U10697		Hsp:LIVER CARBOXYLESTERASE 4 PRECURSOR	R.norvegicus mRNA for pl esterase (ES-4)
17291	, u	931	931 A1172491	Citrate cycle (TCA cycle), Glutathione metabolism	HHs:isocitrate dehydrogenase 2 (NADP+), mitochondrial	ESTs, Weakly similar to IDHC_RAT ISOCITRATE DEHYDROGENASE IR.norvegicus]
17324 A	A	1686	1686 NM 021593			Rattus norvegicus kynurenine 3- hydroxylase mRNA, complete cds
17334 A	4	151	151 AA858704			ESTs, Highly similar to responsible for hereditary multiple exotosis [M.musculus]
17335 A	4	732	732 AI102634			ESTs, Weakly similar to W06B4.2 [C.elegans]
17337		472	472 AB000717	Methionine metabolism, Selenoamino acid metabolism	HHs:methionine adenosyltransferase II, aloha	ESTS
17339 A	A	123				ESTs
17340 A,E	A,E	205	507 AI007803			Rattus norvegicus ERM-binding phosphoprotein mRNA, complete cds
17368 E,R	E,R	284	284 AA900548			ESTs
17369 C,I,P	C,I,P	812	812 AI137572	-		ESTs
17377 A	A	1491	1491 X13058		Tumor protein p53 (Li-Fraumeni syndrome)	Rat mRNA for nuclear oncoprotein p53
17393 A,O	A,O	1377	1377 J04943		Nucleoplasmin-related protein (Nuclear Nucleoplasmin-related protein (Nuclear protein B23	Nucleoplasmin-related protein (Nuclear protein B23
17400 E	Ш	744	744 AI103097			ESTs, Highly similar to ATPK_MOUSE ATP SYNTHASE F CHAIN, MITOCHONDRIAL [M.musculus]
17401 A	A	1595	1595 NM_013043		Transforming growth factor beta stimulated clone 22	Transforming growth factor beta stimulated clone 22

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Document Number 1650775	. 192	Unigene Cluster Title	ESTs, Highly similar to DHYS_HUMAN	DEOXYHYPUSINE SYNTHASE	[H.sapiens]	ESTs	R.norvegicus mRNA for RT1.Ma	ESTs	Rattus norvegicus sodium-dependent	high-affinity dicarboxylate transporter	(NADC3) mRNA, complete cds	ESTs	iron-responsive element-binding protein iron-responsive element-binding protein	ESTs	Epoxide hydrolase 1 (microsomal	xenobiotic hydrolase)	Rattus norvegicus mRNA for hnRNP	protein, partial	Rattus norvegicus mRNA for hnRNP	protein, partial	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to FKB1_RAT	FK506-BINDING PROTEIN	[R.norvegicus]	ESTs	ESTs
	Fefter	Known Gene Name											iron-responsive element-binding protei		Epoxide hydrolase 1 (microsomal	xenobiotic hydrolase)													
		Pathways																											
	GenBank	Acc ID			806 AI137356	AI145385	1529 249761	325 AA926109			1713 NM_022866	649 AI070068	1739 NM_017321	539 AI010568	770070	1580 NM 012844		1276 AI236484		71 AA818524	248 AA892851	248 AA892851	898 AI171354	10 AA799511			1269 AI236301	293 AA924036	1238 AI234496
	Nuc Seq	0			806	827	1529	325			1713	649	1739	539	7	1580	į	1276		71	248	248	868	10			1269	293	1238
E 1	GLGC Comparison	Code			Е	R	Е	A			I,P	7	0	A		G,K		H,-		Ш	٧	±	А	0			ш	Я	B,Q
TABLE 1	OFTO	-			17451 E	17479 R	17481 E	17496 A			17500	17506	17516	17524 A	1	1/541 G,K]	17571	•	17572 E	17589 A	17590 F	17591	17613			17617 E	17644 R	17664 B,Q

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TABLE 1						Document Number 1650775
	7200	Nucleotide				
	40030E9	Ostraelice	Acc ID	Pathways.	Known Gene Name	Unigene Cluster Tifle
						ESTs, Highly similar to NIMM_MOUSE
	-			Oxidative phosphorylation	HMm:NANH	NADH-UBIQUINONE
17672 N		1123	1123 AI230074	Ubiquinone biosynthesis	oxidoreductase subunit MWFE	M.musculus]
17677 E		683	683 AI072246			ESTs
17683 N		700	700 AI073257			ESTs
0		6				Rat mRNA for dimethylglycine
17684 G		236	236 AA892345			dehydrogenase (EC number 1.5:99.2)
17685 K		797	797 AI113055			EST
	•					ESTs, Weakly similar to predicted using
17687 C		12	12 AA799531			Genefinder [C.elegans]
						ESTs, Weakly similar to predicted using
17688 A		12	12 AA799531			Genefinder [C.elegans]
						ESTs, Weakly similar to putative
				7		peroxisomal 2,4-dienoyl-CoA reductase
17695 N		1192	1192 AI232784			[R.norvegicus]
1						ESTs, Weakly similar to NG28
17699 O		135	135 AA851233			[M.musculus]
17709 A		1456	1456 U24489		Tenascin X	Tenascin X
17730 G		1709	1709 NM_022697			Rat mRNA for ribosomal protein L28
						ESTs,Rattus norvegicus heat shock
17734 C,D		466	466 AA998683			protein 27 (hsp 27) gene, complete cds
				_		ESTs, Rattus norvegicus heat shock
17735 C,D,J		981	981 AI176658			protein 27 (hsp 27) gene, complete cds
(,			ESTs,Rattus norvegicus heat shock
17736 C,D		1428	1428 M86389			protein 27 (hsp 27) gene, complete cds
						ESTs. Highly similar to cellular apoptosis
17747 E		1236	1236 AI234223			susceptibility protein [H.sapiens]

Document Number 1650775		Unigene Cluster Title	ESTs, Highly similar to S65568 CCAAT-	binding factor CBF2 - mouse	[M.musculus]	ESTs, Highly similar to vacuolar H- ATPase subunit D IH.sapiensl								Rat peroxisomal enoyl-CoA: hydrotase-3	hydroxyacyl-CoA bifunctional enzyme	mRNA, complete cds	ESTs	polipoprotein C-III	ESTs, Highly similar to sid478p	M.musculus]							ESTs	ESTs	Rat ribosomal protein L30 mRNA,	complete cds
		Known Gene Name	<u> </u>	ia		三 日 (Y						•		HHs:enoyl-Coenzyme A, hydratase/3-			<u> </u>	Apolipoprotein C-III		Esterase D/formylglutathione hydrolase [[M.musculus]						metabolism, One carbon pool HHs:serine hydroxymethyltransferase 1	(soluble)		<u> </u>	<u> </u>
		Pathways						Butanoate metabolism, Fatty	acid biosynthesis (path 2),	Fatty acid metabolism,	Lysine degradation,	Propanoate metabolism.	Tryptophan metabolism.		isoleucine degradation, beta-hydroxyacyl Coenzyme A	Alanine metabolism					Cyanoamino acid	metabolism, Glycine, serine	and threonine	metabolism,Lysine	degradation, Methane	metabolism, One carbon pool	by folate			
	GenBank	AccID			748 AI103246	261 <u>AA893246</u>	0470000									1645 NM 017220	774 AI105196	1534 NM 012501		271 AA899045							772 AI105184	262 AA893436		5 AA686461
	見る				748	264	102									1645	774	1534		271							772	262		5
E.1	GLGC Comparison	Code			3		_							•		<u>≈</u>	3 B	Z		<u>×</u>							E,N	N) <u>B</u>
TABLE 1	29.19	9			17753	17754	5									17758 G	17768	17785 N		17788 K							17794	17800 N		17809 B

TABLE 1					Document Number 1650775
***		otide			
	Code ID) Pathways	Known Gene Name	Unigene Cluster Title
			Glutathione metabolism,	HMm:glutathione transferase zeta 1	
17812 A,E		841 AI169075	Tyrosine metabolism	(maleylacetoacetate isomerase)	ESTs
					ESTs, Highly similar to unknown
17819 A		891 AI171095			[H.sapiens]
17844 A,E		398 AA955927			ESTs
17847 A		1025 AI178214			ESTs
					ESTs, Weakly similar to TCPA_RAT T-
					COMPLEX PROTEIN 1, ALPHA
17850 A		734 AI102750			SUBUNIT [R.norvegicus]
					Rat mRNA for MRC OX-45 surface
17854 Q		1490 X13016			antigen
17894 E,F		1594 NM_013027	72	Selenoprotein W muscle 1	Selenoprotein W muscle 1
				interferon-related developmental	interferon-related developmental
17908 A,J		1670 NM_019242	12	regulator 1	regulator 1
					Rattus norvegicus membrane interacting
					protein of RGS16 (Mir16) mRNA,
17935 S		289 AA901006			complete cds
				myeloid differentiation primary	
17950 Q		1278 AI236590		response gene 88	ESTs
17955 L		590 AI030069			ESTs
				adaptor-related protein complex AP-1,	adaptor-related protein complex AP-1,
17956		427 AA964379		beta 1 subunit	beta 1 subunit
					Glutamate receptor, ionotropic, N-methyl
				Glutamate receptor, ionotropic, N-	D-aspartate 1,Rat N-methyl-D-aspartate
17982 A		1727 NM_017010	- 01	methyl D-aspartate 1	receptor (NMDAR1) gene, first exon

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	Document Number 1650775	ESTs, Highly similar to SP24_RAT SECRETED PHOSPHOPROTEIN 24 [R.norvegicus], Rattus norvegicus spp-24	ESTs, Highly similar to SP24_RAT SECRETED PHOSPHOPROTEIN 24 [R.norvegicus], Rattus norvegicus spp-24	Rattus norvegicus UDP- glucuronosyltransferase UGT1A7	Sex hormone binding globulin or androgen-hinding protein	Rattus norvegicus progression elevated gene 3 profein mRNA complete cds	Rattus norvegicus versican V0 isoform mRNA, partial cds,Rattus norvegicus versican V3 isoform precursor, mRNA,	complete cds R.norvegicus mRNA for mitochondrial	R.norvegicus mRNA for mitochondrial	ESTs, Highly similar to A60054 sodium channel protein IIIb, long form - rat	R.norvegicus mRNA for ribosomal protein L14
	Known Gane Name		BEST SEC P. C.	Ratt	Sex hormone binding globulin or Sex androgen-binding protein		Ratti mRN vers	Com R.no	Very- HSP:ACYL COENZYME A THIOESTER HYDROLASE, MITOCHONDRIAL R.no PRECURSOR	ESTE	R.no prote
	Pathways							-	1 1 0		
	de GenBank Acc ID	149 AA858573	600 AI043655	1337 D38062	1418 M38759	487 AF020618	500 AE072892	478 AB010429	1524 Y09333	1604 NM 013119	1717 NM 022949
	Nucleotide son Sequence ID	14	09	133	141	48	20	478	1524	1604	1717
TABLE 1	SC Comparison Code	18001 A	18002 A,D,E	9	8 6	3.7		2.5	8	9	
TAB	GLGC D	1800	1800	18028 G	18029 S	18043	18046	18082 S	18083	18099	18107

GLGC Comparison Nucleotide ID Code ID 18109 A 1577 18115 A 31 18125 S 515	tide GenBank Acc.ID 577 NM_012823 31 AA800339 515 Al008787	Patriways	Known Gene Name (1)	ESTs. Weakly similar to LURT3 annexin ESTs
<u> </u> 4	737 AI102820 1014 AI177413		ATP synthase subunit d	ESTs ATP synthase subunit d,ESTs, Weakly similar to myo-inositol-1-phosphate synthase ID melanogasterl
41	1584 NM_012891			ESTs, Highly similar to ACDV_RAT ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR [R.norvegicus]
ထ ပ	758 AI104523 1065 AI179539			ESTs ESTs, Highly similar to CDC45L [M.musculus]
0	1280 Al236601 6 AA799294			ESTs ESTs, Moderately similar to KIAA0740 protein [H.sapiens]
4 1	384 AA946361 341 AA943791			ESTs, Highly similar to Ring3 [M.musculus] ESTs
6	499 AF072411			Rattus norvegicus FAT mRNA, complete cds
35	385 AA946368 556 Al012498			Rattus norvegicus FAT mRNA, complete cds
N	22 AA799744			ESTs

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Document Number 1650775	Unigene Cluster Title	Rattus norvegicus phospholemman chloride channel mRNA, complete cds	Rattus norvegicus brain natriuretic	peptide (BNP) mRNA, complete cds	ESTs	ESTs					CTL target antigen					CTL target antigen	ESTs	ESTs	ESTs, Highly similar to pinin [H.sapiens]	ESTs, Highly similar to KIAA0184 [H saniens]	ESTS	Rat calbindin D28 mRNA, complete cds	ESTs	ESTs	ESTs	ESTs
	Known Gene Name			Brain natriuretic factor						•	CTL target antigen					CTL target antigen										
	Pathways						Cysteine metabolism,	Methionine metabolism,	Nitrogen metabolism,	Selenoamino acid	metabolism	Cysteine metabolism,	Methionine metabolism,	Nitrogen metabolism,	Selenoamino acid	metabolism										
	GenBank Acc ID	19 AA799645		9 AA799498	128 AA850038	969 AI176483					1630 NM_017074					1630 NM_017074	1077 AI180187	838 AI168975	1311 AI639151	1249 AI235349	1307 AI639042	1414 M31178	830 AI145870	1136 AI230716	142 AA851963	216 AA891694
	Nucleotide Sequence ID	19,		6	128	696					1630					1630	1077	838	1311	1249	1307	1414	830	1136	142	216
1	GLGC Comparison ID Code	9		A,B,Q	A,E	၁					۷					A	B,Q	K	I		В	_	A,E	B,Q	M,P	I
TABLE	OLGC GLGC	18369 G		18389 A,B,Q	18390 A,E	18418 C					18452 A					18453 A	18465 B,Q	18473 K	18482 H	18484	18495 B	18501	18522 A,E	18529 B,Q	18580 M,P	18584 H

TABLE 1	1					Document Number 1650775
D G	omparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
						ESTs, Moderately similar to 2020285A
18588 E	Ш	7/0	276 AA899635			DRG i protein [ivi.muscuius]
				Nucleotide sugars		
				metabolism, Pentose and		
				glucuronate		
				interconversions, Starch and		Rattus norvegicus mRNA for UDP-
18597 A	<	481	481 AB013732	sucrose metabolism	HMm:UDP-glucose dehydrogenase	glucose dehydrogeanse, complete cds
18604 N	z	1292	1292 AI237124			ESTs
						ESTs, Highly similar to RL12_RAT 60S
						RIBOSOMAL PROTEIN L12
18606 A	4	1497	1497 X53504			[R.norvegicus]
						ESTs, Highly similar to RL23_HUMAN
						60S RIBOSOMAL PROTEIN L23
18612 E,O	E,O	1092	1092 AI228624			[R.norvegicus]
						ESTs, Weakly similar to HS9B_RAT
						HEAT SHOCK PROTEIN HSP 90-BETA
18647 E	Ш	1435	1435 S69316			[R.norvegicus]
18660 A	A	894	894 AI171262		cyclin G2	ESTs
18661 A	<	376	376 AA945751			ESTs
					dodecenoyl-Coenzyme A delta	dodecenoyl-Coenzyme A delta
					isomerase (3,2 trans-enoyl-Coenyme A	isomerase (3,2 trans-enoyl-Coenyme A isomerase (3,2 trans-enoyl-Coenyme A
18685		453	453 AA997746	Fatty acid metabolism	isomerase)	isomerase)
18705		1732	1732 NM 020103		Ly6-C antigen gene	Ly6-C antigen gene
				Alanine and aspartate metabolism, Arginine and		
				proline metabolism, Urea		
				cycle and metabolism of		Rat mRNA for argininosuccinate lyase,
18727 S	S	1685	1685 NM_021577	amino groups	HHs:argininosuccinate lyase	complete cds

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寻览	Nucleotide Sequence	GenBank			229
	9	AccilD	Pathways	Known Gene Name	Unigene Cluster Title
					ESTs, Highly similar to AF189764_1
	1697	769 AI105131			alpha/beta hydrolase-1 [M.musculus]
_	006	900 AI171506	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
	1550	1550 NM 012600	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
	1550	1550 NM_012600	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
L	1279	1279 AI236599			ESTs
L	1282	1282 AI236746			ESTs
_	, 299	662 AI071177			ESTs
	1483	1483 U95001			ESTs
	45	45 AA817761			ESTs
-	84	84 AA818796			ESTs
-					ESTs, Moderately similar to
					PLTP_MOUSE PHOSPHOLIPID
					TRANSFER PROTEIN PRECURSOR
	901	901 AI171583			[M.musculus]
					ESTs, Weakly similar to N-copine
	1300	1300 AI237636			[M.musculus]
\vdash					Rattus norvegicus mRNA for
					hydroxysteroid sulfotransferase subunit,
	861	861 AI169695			complete cds
			Androgen and estrogen		Rattus norvegicus mRNA for
			metabolism, Sulfur	Hsp:ALCOHOL	hydroxysteroid sulfotransferase subunit,
	1329	1329 D14989	metabolism	SULFOTRANSFERASE	complete cds
_					Rattus norvegicus mRNA for serine
	1348	1348 D88250			protease, complete cds
	989	686 AI072393			ESTs
					ESTs, Highly similar to AF157028_1
					protein phosphatase methylesterase-1
	583	583 AI029827			[H.sapiens]

Document Number 1650775	Unigene Cluster Title	ESTs,ESTs, Highly similar to	AF157028_1 protein phosphatase	methylesterase-1 [H.sapiens]	ESTs	ESTs	ESTs, Highly similar to PSD8_HUMAN	SUBUNIT S14 [H.sapiens]	ESTs, Highly similar to NADH-	ubiquinone oxidoreductase NDUFS2	subunit [H.sapiens]	ESTs, Moderately similar to PTD012	[H.sapiens]	ESTs	ESTs	ESTs						Acetyl-Co A acetyltransferase 1,	mitochondrial	ESTs
	Known Gene Name								HHs:NADH dehydrogenase	phosphorylation, Ubiquinone (ubiquinone) Fe-S protein 2 (49kD)	(NADH-coenzyme Q reductase)											Acetyl-Co A acetyltransferase 1,	mitochondrial	
	Pathways								Oxidative	phosphorylation, Ubiquinone	biosynthesis						Bile acid biosynthesis, Butanoate metabolism, Fatty	acid biosynthesis (path 2), Fatty acid metabolism.	Lysine degradation,	Propanoate metabolism,	Pyruvate metabolism, Synthesis and degradation	of ketone bodies,	Tryptophan metabolism	
	e GenBank Acc ID			340 AA943785	280 AA899964	303 AA924598		1214 AI233570			883 AI170770		243 AA892561	122 AA849426	122 AA849426	1182 AI232419							1631 NM_017075	1004 A1177103
	Nucleotide rison Sequence le ID			37	28	3(12,			₩ —		5	7	1,	118							16.	10
TABLE1	GLGC Comparison ID Code			18886 R	18890 B,P,S	18891 B,Q,S		18900 F			18905 E		18906 A,K	18908 A	18909 A	18910 A			•••				18956 S	18960 A

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	Mirelantida		The statement of the st		
GLGC Comparison ID Code	Sequence	GenBank AccID F	Pathways	Known Gene Name	Unigene Cluster Title
					Rattus norvegicus TM6P1 (TM6P1)
	574	574 AI013918			mRNA, complete cds
18974 M	319	319 AA925384			EST
I	11	11 AA799523			ESTs, Moderately similar to hnRNP protein [R.norvegicus]
18990 G	1438	1438 S72506	Glutathione metabolism	Glutathione-S-transferase, alpha type (Yc?)	Glutathione-S-transferase, alpha type (Yc?)
N 9681	1027	1027 AI178326			ESTs
19012 J,K	918	918 AI172056			ESTs
	107	10000			Rat S-100 related protein mRNA,
	13/4	13/4 J0362/			complete cds, clone 42C
19043 F	130	130 AA850378			ESTS, Rightly Similar to memyl-cho binding protein MBD2 [M.musculus]
		0			ESTs, Highly similar to methyl-CpG
19044 S	1253	380 AA9463/9			binding protein MBDZ [M.musculus]
,,:	202	0.000			Rattus norvegicus mRNA for
					mitochondrial adenine nucleotide
19053 K	1327	1327 D12770			translocator
19069 A,L	339	339 AA943737			ESTs
ш	34	34 AA800576			ESTs
					ESTs, Moderately similar to cysteine-rich
19075 B,J	1275	1275 AI236473			hydrophobic 1 [M.musculus]
19085 A,J	244	244 AA892598			ESTs
19086 A,J	244	244 AA892598			ESTs
19103 A	36	36 AA800797			ESTs
					ESTs, Highly similar to HG14_MOUSE NONHISTONE CHROMOSOMAL
19105 E	162	162 AA859230			PROTEIN HMG-14 [M.musculus]

TABLE1		Box of the second			Document Number 1650775
	Nucleotide				
D Code	OI	Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
19121 P	√ 809 ∀	608 AI044101			ESTs
19150 C	∀ 8	8 AA799461			ESTs
					ESTs, Moderately similar to hypothetical
19158 B	140	140 AA851953			protein [H.sapiens]
					ESTs, Highly similar to TGIF_MOUSE 5'-
					TG-3' INTERACTING FACTOR
19184 J	1022	1022 AI178025			[M.musculus]
19211 N	136	136 AA851329			ESTs
19230 R	646	646 AI059604			ESTs
19241	1666 N	1666 NM_019206		Serine/threonine kinase 10	Serine/threonine kinase 10
19252 N	2	NM_019382		anti-oxidant protein 2	anti-oxidant protein 2
					Rat (diabetic BB) MHC class II alpha
19255 K	1406 N	1406 M15562			chain RT1.D alpha (u)
					Rat (diabetic BB) MHC class II alpha
19256 K	1406 N	1406 M15562			chain RT1.D alpha (u)
19258 O	287	287 AA900613			ESTs
19261 0	741	741 AI102943			ESTs
19264 C,D,R	743	743 AI103078			ESTs
19292 K	7 442	445 AA997323			EST
					ESTs, Weakly similar to NHPX_RAT
					NHP2/RS6 FAMILY PROTEIN
19298 A,D,I	1272	1272 AI236338			YEL026W HOMOLOG [R.norvegicus]
19315 E	1144	1144 AI231010			EST
					ESTs, Moderately similar to unnamed
19363 A,F	954 /	954 AI176247			protein product [H.sapiens]
19373 N	1684 N	1684 NM 021266		Hyaluronan mediated motility receptor (RHAMM)	Hyaluronan mediated motility receptor (RHAMM)

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TABLE						Document Number 1650775
0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	GLGC Comparison ID Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	. Unigene Cluster Title
						ESTs, Moderately similar to RL3_RAT
						60S RIBOSOMAL PROTEIN L3
19377		180	180 AA859971			[R.norvegicus]
19388	Ш	206	206 AA891032			EST
				Arginine and proline metabolism, Biosynthesis		
				and degradation of	Protein disulfide isomerase (Prolyl 4-	Protein disulfide isomerase (Prolyl 4-
19392 M	Σ	1592	1592 NM_012998	glycoprotein	hydroxylase, beta polypeptide)	hydroxylase, beta polypeptide)
						ESTs, Moderately similar to
						AC006978_1 supported by human and
19410 B,Q	B,Q	268	268 AA893667			rodent ESTs [H.sapiens]
						ESTs, Moderately similar to
						AC006978_1 supported by human and
19411 M,P	M,P	268	268 AA893667			rodent ESTs [H.sapiens]
						ESTs, Moderately similar to
						AC006978_1 supported by human and
19412 B,Q	B,O	120	120 AA849222			rodent ESTs [H.sapiens]
19444 P	Ь	608	309 AA924993			ESTs
19458 E	Ш	462	462 AA998345			EST
19465 K	*	020	630 AI045881			EST
						ESTs, Weakly similar to proline
19469 A,P	A,P	231	231 AA892112			dehydrogenase [M.musculus]
						ESTs, Weakly similar to proline
19470 A	4	1203	1203 AI233266			dehydrogenase [M.musculus]
19476 0	0	1188	188 AI232612			ESTs
						ESTs, Moderately similar to vascular
19503 P	Р	116	116 AA848639			endothelial growth factor D [M.musculus]
19508 A	A	1114	1114 AI229698			EST

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Document Number 1650775	Rattus norvegicus adipocyte lipid-binding protein (ALBP) mRNA, complete cds	ESTs	ESTs, Highly similar to ATP binding protein [H.sapiens]	ESTs	EST	EST	ESTs,Rattus norvegicus retinoid X	receptor gamma (RXRgamma) mRNA, partial cds	Rattus norvegicus mRNA for SH2-	containing inositol phosphatase 2	(SHIP2), complete cds		subunit B, alpha isoform (calcineurin B, protein phospatase 3, regulatory subunit	B, alpha isoform (calcineurin B, type I)	Rat mRNA for type I thyroxine	deiodinase	Rat mRNA for type I thyroxine	deiodinase	membrane cofactor protein	ESTs	ESTs	ESTs	EST	ESTs	ESTs
Known Gene Name												protein phospatase 3, regulatory	subunit B, alpha isoform (calcineurin B,	type I)		Thyroxine deiodinase, type I		Thyroxine deiodinase, type I	membrane cofactor protein						
ink Daffways			6	4	2						944			608		653		653	190	4	0	3	13	73	4
Nucleotide Sequence GenBank	855 AI1	1100 AI229035	112 AA819879	559 AI012747	97 AA819172	663 AI071181		486 AF016387			1740 NM 022944			1656 NM_017309		1733 NM_021653		1733 NM_021653	1662 NM 019190	872 AI170394	87 AA818910	1262 AI236066	272 AA899113	237 AA892373	1304 AI638994
GLGC Comparison S		19513 R	19566 E	19591 S	19605 E,L	19641 J		19650 H			19669 R			19671 B,Q		19678 A		19679 A	19715 M	19728 0	19729 A	19732 A,G	19762 R	19768	19787 H

TABLE 4				The second secon		Document Number 1650775
00/0	nosiisono	Nucleotide	JueBuet	14, 	Trans	
} =	700.303	OI OI	Accil	Pathways	Known Gene Name	Unigene Cluster Title
				Taurine and hypotaurine	HHs:cysteine sulfinic acid	Rattus norvegicus brain mRNA for
19824 0	0	1688	1688 NM_021750	metabolism	decarboxylase-relatedprotein 2	cysteine-sulfinate decarboxylase
				Taurine and hypotaurine	HHs:cysteine sulfinic acid	Rattus norvegicus brain mRNA for
19825	0	1688	1688 NM 021750	metabolism	decarboxylase-relatedprotein 2	cysteine-sulfinate decarboxylase
						ESTs, Weakly similar to 305B_RAT 3-
					-	OXO-5-BETA-STEROID 4-
19830 A	4	853	853 AI169529			DEHYDROGENASE [R.norvegicus]
19843 A	A	1308	1308 AI639055			EST
19909 A	A	1315	1315 AI639310			EST
						ESTs, Moderately similar to pescadillo
19940 C	ပ	1254	1254 AI235689			[H.sapiens]
19952 A	A	1310	1310 AI639108			ESTs
						ESTs, Moderately similar to dJ967N21.3
20016 B	В	1312	1312 AI639158			[H.sapiens]
						Rattus norvegicus Nopp140 associated
20035 A	∢	1689	689 NM_021754			protein (NAP65) mRNA, complete cds
20038 S	S	278	278 AA899797			EST
20041 K	7	787	787 AI112161			ESTs
						ESTs, Highly similar to R32184_3
20063 E,L	E,L	313	313 AA925063			[H.sapiens]
						EST, Highly similar to A42772 mdm2
20082 C	O	1316	1316 AI639488			protein - rat [R.norvegicus]
20088 A	A	246	246 AA892666			ESTs
						Rattus norvegicus pleiotropic regulator 1
20090 R	<u>~</u>	1690	1690 NM_021757			(PLRG1) mRNA, complete cds
						EST, Moderately similar to
						TNFC_MOUSE LYMPHOTOXIN-BETA
20119 P	Ь	1033	1033 AI178533			[M.musculus]

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TARIF1						Document Number 1650775
		Nucleotide		12 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
0 0 0	GLGC Comparison	Sequence	Genbank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
						Rattus norvegicus EH domain binding
20134 P	<u>a</u>	1692	1692 NM 021852			protein epsin 2 mRNA, complete cds
20161 A.B	A,B	1691	1691 NM 021836			R.norvegicus pJunB gene
						Rat interleukin 1 receptor antagonist
20200 M	Σ	1693	1693 NM_022194			gene, complete cds
					glycerol-3-phosphate acyltransferase,	glycerol-3-phosphate acyltransferase,
20282 H	Ξ	1648	1648 NM_017274	Glycerolipid metabolism	mitochondrial	mitochondrial
						Rattus norvegicus gene for L-gulono-
20299 A,D	A,D	1694	1694 NM_022220			gamma-lactone oxidase
20350 L.Q	l.o	1186	1186 AI232552			EST
					K-kininogen, differential splicing leads	K-kininogen, differential splicing leads to
20354 B,N,Q	B,N,Q	1404	1404 M14369		to HMW Kngk	HMW Kngk
						Rattus norvegicus mRNA for ATP-
						stimulated glucocorticoid-receptor
20380 E.G	E.G	1330	1330 D16102	Glycerolipid metabolism	glycerol kinase	translocaton promoter, complete cds
						ESTs, Moderately similar to
						SYM_HUMAN METHIONYL-TRNA
20397 A.E	Ą.E	1151	1151 AI231226			SYNTHETASE [H.sapiens]
						Rattus norvegicus JE/MCP-1 mRNA,
20449 A.C.	A,C,I	1494	1494 X17053		Small inducible gene JE	complete cds
20456 A.C	A.C	1355	1355 H31144			ESTs
						Rattus norvegicus mRNA for organic
						anion transporting polypeptide 4
20502 A.F	Ą.F	370	370 AA945533			(slc21a10 gene)
						Rattus norvegicus mRNA for organic
						anion transporting polypeptide 4
20503	20503 A,C,E	864	864 AI169779			(slc21a10 gene)

Document Number 1650775	Unigene Cluster Title	Pvruvate kinase, liver and RBC	ESTs, Moderately similar to podocalyxin [R.norvegicus]	ESTs, Moderately similar to podocalyxin [R.norvegicus]	lipopolysaccharide binding protein	Rattus norvegicus carnitine octanoyltransferase mRNA, complete	cds	sodium channel, voltage-gated, type I,	peta polypeptide	Protein 9 Ka homologous to calcium-	binding protein	Arginosuccinate synthetase 1	ESTs, Highly similar to SRPR_HUMAN SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT	[H.sapiens]	Cytochrom P450	ESTs	ESTs
	Known Gene Name	Pyrnyate kinase, liver and RBC			lipopolysaccharide binding protein	4.		sodium channel, voltage-gated, type I,	beta polypeptide	Protein 9 Ka homologous to calcium-	binding protein	Arginosuccinate synthetase 1			Cytochrom P450		
The state of the s	Pathways	Glycolysis/ Gluconeogenesis, Purine metabolism, Pyruvate										Alanine and aspartate metabolism, Arginine and proline metabolism, Urea cycle and metabolism of amino groups					
	GenBank Acc ID #S	1554 NM 012624	224 AA891842	224 AA891842	1644 NM 017208		1458 U26033		1654 NM_017288		1553 NM_012618	1489 X12459		996 AI1 76990	U36992	H32977	442 AA997048
	Nucleotide Sequence ID	1554	224	224	1644		1458		1654		1553	1489		966	1460	1361	442
TABLE 1	GLGC Comparison	20513 A	20522 P	20523 C,P	20529 F,M,P		20555 G	4	20579 0		20589	20597 S		20644	20651 P	20684 C	20694 A

TABLE 1	A STATE OF THE STA				Document Number 1650775
	Nucleotide			- 10 A	
GLGC Comparison Sequence		GenBank Acc ID	Pathways	Known Gene Name	Unidene Cluster Title
z	1519 X86561	6561			Rat alpha-fibrinogen mRNA, 3' end
20701 A,B,F,Q	197 AA	197 AA875097			Rat alpha-fibrinogen mRNA, 3' end
			Fatty acid	Cytochrome P450, subfamily I	Cytochrome P450, subfamily I (aromatic
			metabolism, Tryptophan	(aromatic compound-inducible),	compound-inducible), member A2 (Q42,
20705 A,D	1541 NN	1541 NM_012541	metabolism	member A2 (Q42, form d)	form d)
					Rattus norvegicus brain digoxin carrier
20707 A,D,K	1481 U88036	8036			protein mRNA, complete cds
					Rattus norvegicus mRNA for NORBIN,
20708 C,F	476 AB	476 AB006461			complete cds
			Fatty acid metabolism,	Cytochrome P450, subfamily IVB,	Cytochrome P450, subfamily IVB,
20711 E,K	1622 NN	1622 NM_016999	Tryptophan metabolism	polypeptide 1	polypeptide 1
			Fatty acid metabolism,	Cytochrome P450, subfamily IVB,	Cytochrome P450, subfamily IVB,
20713 K	1622 NN	1622 NM 016999	Tryptophan metabolism	polypeptide 1	polypeptide 1
			Fatty acid metabolism,	Cytochrome P450, subfamily IVB,	Cytochrome P450, subfamily IVB,
20714 K	1622 NN	1622 NM_016999	Tryptophan metabolism	polypeptide 1	polypeptide 1
			Fatty acid metabolism,	Cytochrome P450, subfamily IVB,	Cytochrome P450, subfamily IVB,
20715 E,N	1622 NN	1622 NM_016999	Tryptophan metabolism	polypeptide 1	polypeptide 1
				antigen identified by monoclonal	antigen identified by monoclonal
20734 A	1672 NM	1672 NM_019283		antibodies 4F2	antibodies 4F2
				antigen identified by monoclonal	antigen identified by monoclonal
20735 A,C,D	1672 NN	1672 NM_019283		antibodies 4F2	antibodies 4F2
20741 F	502 AF	502 AF084186			R.norvegicus mRNA for alpha II spectrin

Document Number 1650775	Unigene Cluster Title	1, Glutamic-oxaloacetic transaminase 1,	soluble (aspartate aminotransferase, cytosolic) see also D1Mgh12	Cyclin G1	Cyclin G1	Rattus norvegicus protein arginine N-	methyltransferase (PRMT1) mRNA, complete cds	ESTs, Moderately similar to HS9B RAT	HEAT SHOCK PROTEIN HSP 90-BETA	[R.norvegicus]	Murine leukemia viral (v-raf-1) oncogene homolog 1 (3611-MSV)		Rattus norvegicus Sprague-Dawley transketolase mRNA complete cds	Rattus norvegicus Sprague-Dawley	transketolase mRNA, complete cds	ESTs, Highly similar to RL1X_RAT 60S RIBOSOMAL PROTEIN L18A	[R.norvegicus]
	Known Gene Name	Glutamic-oxaloacetic transaminase 1,	soluble (aspartate aminotransferase, cytosolic) see also D1Mgh12	Cyclin G1	Cyclin G1						egf,epo,il2,il3,il6,insulin,inter Murine leukemia viral (v-raf-1) act6-1,ngf,pdgf,tpo oncogene homolog 1 (3611-MSV)	Apurinic/apyrimidinic endonuclease 1	HMm-transketolase		HMm:transketolase		
	Pathways	Alanine and aspartate metabolism, Arginine and proline metabolism, Cysteine metabolism, Glutamate metabolism, Phenylalanine metabolism, Phenylalanine, tyrosine and	tryptophan biosynthesis, Tyrosine metabolism								egf,epo,il2,il3,il6,insulin,inter act6-1,nqf,pdqf,tpo		Denfose phosphate cycle		Pentose phosphate cycle		
	GenBank Acc (D		1545 NM 012571	NM_012923	1587 NM 012923		1468 U60882			355 AA944397	1405 M15428	1723 NM 024148	1707 NM 022592		1707 NM_022592		1493 X14181
	Nucleotide Sequence ID		1545	1587	1587		1468			355	1405	1723	1707		1707		1493
1	omparison Code		¥		A		A H				I	A,I	Y		ᆇ		٥
TABLE	GLGC		20744 K	20755	20757		20772 A F			20795	20799 H	20801 A,	71 60000	70002	20804 K		20810

Document Number 1650775	Section 1	Unigene Cluster Title	glutathione S-transferase, pi 2	glutathione S-transferase, pi 2	ESTs, Weakly similar to TCPA_RAT T-	COMPLEX PROTEIN 1, ALPHA	SUBUNIT [R.norvegicus]	ESTs, Highly similar to RL2B_HUMAN	60S RIBOSOMAL PROTEIN L23A	[R.norvegicus]	Rat mRNA for myosin regulatory light	chain (RLC)	acyl-CoA hydrolase	Carnitine palmitoyltransferase 1 beta,	muscle isoform	Carnitine palmitoyltransferase 1 beta,	muscle isoform	aflatoxin B1 aldehyde reductase	ESTs, Highly similar to RS19_RAT 40S	RIBOSOMAL PROTEIN S19	[R.norvegicus]	ESTs, Moderately similar to KIAA0952	protein [H.sapiens]	R.norvegicus mRNA for pl 6.1 esterase	(ES-10)	Solute carrier 16 (monocarboxylic acid	transporter), member 1	ESTs, Highly similar to CGI-117 protein	[H.sapiens]	ESTs, Highly similar to Copa protein	[M.musculus]
			glutathione S-transferase, pi 2		S3	3	าร	S3	09	[R	Re	r)	acyl-CoA hydrolase	Carnitine palmitoyltransferase 1 beta, Ca	muscle isoform	Carnitine palmitoyltransferase 1 beta, Ca	muscle isoform	aflatoxin B1 aldehyde reductase afl	33	<u>R</u>	<u></u>	<u> </u>	nd	~	<u>国)</u>	Solute carrier 16 (monocarboxylic acid Sc	transporter), member 1		H	<u> </u>	M]
	34 52.	Pathways	Glutathione metabolism	Glutathione metabolism										Fatty acid metabolism,	Glycerolipid metabolism	Fatty acid metabolism,	Glycerolipid metabolism														
	GenBank	Acc ID	558 AI012589	1485 X02904			13 AA799545			1147 AI231140		1487 X05566	1614 NM 013214		1613 NM 013200		1613 NM_013200	NM 013215			1000 AI177042		1116 AI229789		1511 X65296		1563 NM 012716		852 AI169337		945 AI175812
	Nucleotide Sequence	322/0	558	1485			13			1147		1487	1614		1613		1613	1615 NM			1000		1116		1511		1563		852		945
	GLGC Comparison	Code	ව	ව			C,D			N,		F,I	Ш		S		S	20864 G.K.P			ගු		A		_		₹		20891 A.C,I		
TABLE	2979	9	20817	20818 G			20843 C,D			20846 E,N		20849 F,	20851		20855		20856 S	20864			20873 G		20874		20879		20889 A		20891		20897

Document Number 1650775	eji Li	e 1		e 1		erol 14 alpha-		r to	TRIN		nucleolar RNA	[sn]			ng chain	ng chain		serine protease				e, mu type 2		16 mRNA,		nthase mRNA,	4140	nthase mkinA,
Document N	Unidene Cluster Title	Aldehyde dehydrogenase	(phenobarbitol inducible)	Aldehyde dehydrogenase 1	(phenobarbitol inducible)	Cytochrom P450 Lanosterol 14 alpha-	demethylase	ESTs, Moderately similar to	PLEK_HUMAN PLECKSTRIN	[H.sapiens]	ESTs, Weakly similar to nucleolar RNA	helicase II/Gu [M.musculus]	ESTs	ESTs	Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain	ESTs	ESTs, Weakly similar to serine protease	[R.norvegicus]		ESTs	Glutathione-S-transferase, mu type 2	(Yb2)	Rattus norvegicus NPW16 mRNA,	complete cds	Rat 5-aminolevulinate synthase mRNA,	Olliplete cus	Rat 5-aminolevulinate synthase mKNA,
	Known Gene Name			Aldehyde dehydrogenase 1	(phenobarbitol inducible)	Cytochrom P450 Lanosterol 14 alpha-	demethylase demethylase	<u>Ш</u>	<u>a</u> :			<u>u</u>	<u>H</u>	3	Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain A	Ш	Ш	I.E.		HMm:carnitine acetyltransferase	Glutathione-S-transferase, mu type 2 G	(Yb2)	<u>8</u>	synaptojanin 2 binding protein	<u> </u>	THS:aminolevulinate, delta-, synthase i complete cus	Rat 5-aminole
Her the second s	Pathwave		<u> </u>	<u>d</u>	9	Fatty acid metabolism, C	Tryptophan metabolism d		, , , , , , , , , , , , , , , , , , , 						7	7				Alanine and aspartate	metabolism		Glutathione metabolism (6		εl	Glycine, serine and
	GenBank		1412 M23995		1730 NM_017272		473 AB004096			7 AA799323		15 AA799576	16 AA799599	18 AA799633	619 AI044900	260 AA893242	1041 AI178741		24 AA799803		318 AA925306		1376 J03914		163 AA859241		13/3 JU3190	7017
	Nucleotide Sequence In	•	1412		1730		473			'		15/	16,	18,	619	260	1041		24		318		1376		163		13/3	Ç
A CONTRACTOR OF THE PERSON OF	omparison		8		κα		Ш			_		I	I	E	L.	8	8		S		S		۵		٧		B	
TABLE	GLGC	2	20914 B		20915 K,Q		20930 E			20950		20971 H	20975 H	20980 E	20983	20986 G	20993 R		20998 S		21010 S		21014 P		21025 A		21039 B	L

Document Number 1650775	Unigene Cluster Title	ESTs, Weakly similar to BACR7C10.a	Coto Highingland ADIRE	ES1S, Filgniy Similar to RB24_MOUSE RAS-RELATED PROTEIN RAB-24	[M.musculus]	Rattus norvegicus thioredoxin reductase	(TrxR2) mRNA, nuclear gene encoding	mitochondrial protein, complete cds			-	Acyl-Coenzyme A dehydrogenase, C-4	to C-12 straight-chain	ESTs	ESTs, Weakly similar to predicted using	Genefinder [C.elegans]	Rat angiotensinogen (PAT) gene	Rat angiotensinogen (PAT) gene	ESTs								
	Known Gene Name							thioredoxin reductase 2	•			nydrogenase, C-4	to C-12 straight-chain				Angiotensinogen	Angiotensinogen									
	Pathways								Fatty acid metabolism,	Propanoate metabolism,	Valine, leucine and	isoleucine degradation, beta-	Alanine metabolism														
	GenBank Acc ID	0 10 4 4 7 4 0	AI011/40		943 AI175675			1706 NM_022584					1617 NM_016986	966 AI176472		1289 AI236972	1400 M12112	344 AA943892	114 AA848437	959 AI176298	119 AA848826	383 AA946189	810 AI137488	768 AI105113	709 AI101205	913 AI171772	615 AI044404
	Nucleotide Sequence ID	L 7.7	7		943			1706					1617	996		1289	1400	344	114	959	119	383	810	768	602	913	615
-	GLGC Comparison	-	_		ш			<u>d</u>					¥	A,F		ш	A,H,N	z	A	7	A	4	0,8	工	~	A,E	K,M
TABLE	01.0C		71000		21068 E			21075					21078 K	21088 A,F		21091 E	21097 A,H,N	21098 N	21125 A	21130	21150 A	21157 A	21164 O,S	21175 H	21184 K	21209 A,E	21228 K,M

Document Number 1650775	Unigene Cluster Title		Rat sth mRNA for silencer factor B	ESTs	ESTs	ESTs, Moderately similar to hypothetical	protein [H.sapiens]	EST	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to /prediction	ESTs	Monoamine oxidase B ESTs ESTs ESTs, Highly similar to TALI_MOUSE TALIN [M.musculus] multiple PDZ domain protein complement component 1, q	
	Known Gene Name	Liver activating protein (LAP, also NF-	IL6, nuclear ractor-IL6, previously	(2.0.1 Samuel Brown											Monoamine oxidase B multiple PDZ domain protein complement component 1, q	annount bound to be bed bobined
The second secon	Pathways		Stochold Si	ווסיווויסוממיס- ו											Arginine and proline metabolism, Glycine, serine and threonine metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism	
	GenBank Acc ID		1740 NIM 02412E	1029 AI178491	125 AA849796		1231 AI234090	126 AA849898	258 AA893082	1227 AI233902	129 AA850195	277 AA899721	35 AA800739	375 AA945708	1612 NM 013198 1255 Al235842 37 AA800962 1664 NM 019196	10 10 10 10 10 10 10 10 10 10 10 10 10 1
	Nucleotide Sequence ID		1740	1029	125		1231	126	258	1227	129	277	35	375	1612 1255 37 1664	101
TABLE 1	GLGC Comparison		7,000	21230 K	212751		21281 B,E,M	21285 P	21305 G	21321 H	21341 A,S	21354 S	21380 J	21382 N	21396 A 21414 P 21416 21421 N	21443 P,Q

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Document Number 1650775	Unigene Cluster Title	complement component 1, q	Rathus norvedicus intracellular calcium-	binding protein (MRP14) mRNA,	complete cds	ESTs	ESTs, Weakly similar to tazarotene- induced gene 2 (H saniens)	FSTs	FOT	E318	ESTs	ESTs	ESTs	Rat ribophorin II mRNA	R.norvegicus mRNA for D-3-	phosphoglycerate dehydrogenase	Rattus norvegicus interferon-inducible	protein variant 10 mRNA, complete cds	Rattus norvegicus interferon-inducible	protein variant 10 mRNA, complete cds	Rattus norvegicus interferon-inducible	protein variant 10 mRNA, complete cds	ferredoxin 1	ESTs	CCAAT/enhancerbinding, protein	(C/EBP) delta	CCAAT/enhancerbinding, protein (C/EBP) delta	
	Known Gene Name	complement component 1, q	subcomponent, pera porprepriae											HHs:ribophorin II									ferredoxin 1		CCAAT/enhancerbinding, protein	(C/EBP) delta	CCAAT/enhancerbinding, protein (C/EBP) delta	
	(Pathways													Biosynthesis and degradation of glycoprotein														
	GenBank Acc ID	NIM O40363	NIM 019202		1388 L18948	311 AA925049	064 01476064	137 AA8513/13	410001	1097 AIZ28729	707 AI101159	762 AI104683	146 AA852038	1499 X55298		1521 X97772		1507 X61381		863 AI169751		968 AI176479	1635 NM_017126	222 AA891789		1609 NM_013154	1609 NM 013154	-
	Nucleotide Sequence ID	7027			1388	311	0.554	137	100	1097	707	762	146	1499		1521		1507		863		896	1635	222		1609	1609	
_	GLGC Comparison ID Code		3		M,P	<u>၂</u>		2 <	ر (۲	Z.	В	z	Ш		<u>ن</u> . ق		В		Σ		Σ	В	ပ		P,Q	۵	
TABLE	2979	777	71444		21445 M,P	21458 C	14. 237 80	24407	1/4/7	21535 R	21567 R	21570 B	21574 N	21575		21586 G,		21657 B		21660 M		21661 M	21663 B	21672 C		21682 P,Q	21683 P	1

DPS17BDD D731D1

TABLE 1					Document Number 1650775
GLGC Comparison	Nucleotide n Sequence	GenBank			
ID Code		Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
					ESTs, Weakly similar to coronin-like
21695 A,I	240	240 AA892506			protein [R.norvegicus]
					Rattus norvegicus ADP-ribosylation
21696 C	1724	1724 NM_024152			factor 6 mRNA, complete cds
21707 A,C,E,N	176	176 AA859722			ESTs
			-	Hsp:ENDOTHELIN-CONVERTING	Rat mRNA for endothelin-converting
21709 Q	1334	1334 D29683		ENZYME 1	enzyme, complete cds
21717 E	131	131 AA850480			ESTs
21740 B,M,Q	986	986 AI176810			ESTs
					ESTs, Moderately similar to
21798 K	329	329 AA926365			AF151827_1 CGI-69 protein [H.sapiens]
21799 E	730	730 AI102576			ESTs
					Rattus norvegicus homocysteine
					respondent protein HCYP2 mRNA,
21818	491	491 AF036537			complete cds
21823 E	1119	1119 AI229906			ESTs
					ESTs, Moderately similar to
					Y101_HUMAN HYPOTHETICAL
21893 E	1302	1302 AI237713			PROTEIN KIAA0101 [H.sapiens]
21909 H	210	210 AA891161			ESTs
					Rattus norvegicus 3-hydroxyiso-
21950 G	220	570 AI013861			butyrate mRNA, 3' end
21976 R	379	379 AA946011			ESTs
					Rattus norvegicus insulin-like growth
					factor binding protein complex acid-labile
21977 A,G	1432	1432 S46785			subunit gene, complete cds

Postument Number 1 650775	Pathways Known Gene Name: Unique Cluster Title	Re	factor binding protein complex acid-labile	subunit gene, complete cds	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to predicted using	Genefinder [C.elegans]	ESTs, Highly similar to serine protease	[Lisapiers]	ESTs, Moderately similar to BI54_MOUSE BRAIN PROTEIN I54	[M.musculus]	ESTs	ESTs, Weakly similar to predicted using	Genefinder [C.elegans]	ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to translation	initiation factor eIF6 [M.musculus]	ESTs	ESTS, Moderately similar to	AF 153422_	avronhoenhorlage A [H sanians]
	Nucleotide Sequence GenBank ID Accil) Pa			298 AA924289	264 AA893454	1297 AI237609	390 AA946476	331 AA942726		275 AA899498	00000	1003 Al1//099		727 AI102258	223 AA891790		887 AI170821	521 AI009115	753 AI103730	1031 AI178527	886 AI170820		1268 AI236294	323 AA925869			
TADI 64	omparison			21978 A,M	21980 H	22038 A,C,D	22042 P	22046 S		22051 E		22077 A		22099 A	22124 J		22135 R	22151 B,E,Q	22177 J	22197 A,C	22204 K		22212 A	22224 S			10000

Document Number 1650775	Unigene Giuster Title	Rat IgE binding protein mRNA, complete	cds	ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to G6P1 MOUSE	GLUCOSE-6-PHOSPHATE	ISOMERASE [M.musculus]	ESTs, Weakly similar to es 64	[M.musculus]	ESTs	ESTs	Rattus norvegicus growth response	protein (CL-6) mRNA, complete cds	ESTs	ESTs, Highly similar to FBRL_MOUSE	FIBRILLARIN [M.musculus]	ESTs	ESTs, Weakly similar to T2D7_RAT	TRANSCRIPTION INITIATION FACTOR	TFIID 31 KD SUBUNIT [R.norvegicus]	ESTs, Highly similar to I49523 Mouse	primary response gene B94 mRNA,	3'end - mouse [M.musculus]	ESTs	Alpha-2-macroglobulin	Alpha-2-macroglobulin
	Known Gene Name									Glucoşe phosphate isomerase																		Alpha-2-macroglobulin	Alpha-2-macroglobulin
	Pathways							Glycolysis / Gluconeogenesis, Pentose	phosphate cycle, Starch and	sucrose metabolism																			
e mangelen de de la companya de la c	GenBank Acc ID		702962	345 AA943896	348 AA944157	349 AA944158	1121 AI230046			1156 AI231448		351 AA944269	352 AA944289	353 AA944304		1702 NM_022392	354 AA944380		895 AI171263	1284 AI236761			358 AA944572			731 AI102578	359 AA944823	1531 NM_012488	1531 NM 012488
	Nucleotide Sequence ID		1372	345	348	349	1121			1156		351	352	353		1702	354		895	1284			358			731	326	1531	1531
1	GLGC Comparison		22321 B,I,M,Q	∢	A,Q	S	Я					S	A	L		Ш	S		A,C	٦			∢			22487 A,F,H		M,P	F.M
TABLE	GLGC D		22321	22338 A	22368 A,Q	22370 S	22375 R			22379		22392	22395 A	22397 F		22412 E	22416 S		22432 A,C	22443			22457 A			22487	22503	22512 M,P	22513 F.M

TABLE						Document Number 1650775
		Nucleotide	A CONTRACTOR OF THE STATE OF TH			
09T9	GLGC Comparison	Sednence	GenBank			
9	Code	lD	AccID	Pathways	Known Gene Name	Unigene Cluster Little
22514 M,P	M,P	1531 N	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22515 M	Σ	1531 N	1531 NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22516 M.P	M,P	796 A	796 AI113046		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22531	Ш	361 A	361 AA944943			ESTs
22534 E	Ш	310 A	310 AA925045			ESTs
				Glyoxylate and		
		-		dicarboxylate		ESTs, Weakly similar to SERA_RAT D-3
				metabolism,Pyruvate	HHs:glyoxylate	PHOSPHOGLYCERATE
22540 R	œ	304 A	304 AA924630	metabolism	reductase/hydroxypyruvate reductase	DEHYDROGENASE [R.norvegicus]
22548		364 A	364 AA945031			ESTs
22554	22554 A,E,G,O	366 A	366 AA945076			ESTs
					Hydroxyacid oxidase 1 (glycolate	
22558 A,E	A,E	368 A	368 AA945123		oxidase)	EST
22559 A,D	A,D	839 A	839 AI169007			ESTs
22566 E	Ш	1007 A	1007 AI177122			ESTs
22569 A	A	1073 A	1073 AI179979			ESTs
22570 R	2	369 A	369 AA945238			ESTs
22582 A.G	A.G	1605 N	1605 NM 013120		Glucokinase regulatory protein	Glucokinase regulatory protein
						ESTs, Weakly similar to SPI-2 serine
22598 M	Σ	811 A	811 AI137506			protease inhibitor [R.norvegicus]
						Rattus norvegicus putative peroxisomal
						2,4-dienoyl-CoA reductase (DCR-AKL)
22603 E	Ш	494	494 AF044574			mRNA, complete cds
22619	22619 B.E.Q	531 A	531 Al009825			ESTs
22620 S	S	316 △	316 AA925258			ESTs
22625	ſ	374 4	374 AA945704			ESTs
22679 A	A	332 4	332 AA942731			ESTs
22681 J	٦	357	357 AA944413			ESTs
22683 A	A	970	970 A1176484			ESTs

Document Number 1650775	Known Gene Name Unigene Cluster Title	ESTs	ESTs	ESTs, Highly similar to entactin	[R.norvegicus]	ESTs	ESTS, Highly similar to TS24_MOUSE PROTEIN TSG24 [M.musculus]	ESTs	ESTs	ESTs, Moderately similar to hypothetical protein IH sanians	אין ייי ייי פאטופויון וויסאסולן	Rattus norvegicus small zinc finger-like protein (TIM10) mRNA, complete cds	ESTs	ESTs	ESTs, Moderately similar to CGI-137	protein [H.sapiens]	ESTs, Moderately similar to CGI-137	protein [11.3dpren3]	1013	ESIS	ESTs	ESTs, Moderately similar to cell death	activator CIDE-A [M.musculus]	ESTs	ESTs	ESTs	ESTs
	. Pathways																										
	Sequence Sendann ID AccID 19	1032 AI178531	378 AA945904		1257 AI235948	804 AI137211	283 AA900506	465 AA998660	387 AA946428	V 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	551 AIU12174	1079 AI180367	528 AI009676	227 AA891944		917 AI172041		1045 A11/8819	290 AA301107	290 AA901107	944 AI175790		29 AA800243	328 AA926262	670 AI071578	670 AI071578	777 AI105417
TABLE1	GLGC companson	22695 H	22713 K		22717 L	22722 0	22725 Q	22737 S	22770 A	L	22806 E,Q	22835 L	22840 N	22862 H		22876 C		22877 A,C,D	22897 P	22898 L,P	22906 L,N		22918 B,Q	22928 A,F	22929 A,L	22930 A	22931 A

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Document Number 1650775	Pathways Known Gene Name Unigene Cluster Title	HMm:mitogen activated protein kinase ESTs, Moderately similar to meningioma expressed antigen 11 [H.sapiens]		ESTS	ESTS	ESTS	ESTs, Weakly similar to ACTC_HUMAIN ACTIN, ALPHA CARDIAC	[R.norvegicus]	ESTs	ESTs	ESTS	ESTs, Weakly similar to URB1_RA1	DNA BINDING PROTEIN ONE-DI	(Hval) askinori loud a sistematical	Rattus not vegicus inyaluroringase (inyaluroringase (inyaluroringa))))	ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to mm-Mago [M.musculus]	Mini chromosome maintenance ESTs, Highly similar to cell division deficient 4 homolog (S. cerevisiae) control protein CDC21 [H.sapiens]	ESTS, Weakly similar to UB5D_RAT UBIQUITIN-CONJUGATING ENZYME	
	Nucleotide Sequence GenBank ID Acc ID	764 01104897	1064 AI179519	1128 AI230320	178 AA859933	334 AA942770		1137 AI230743	305 AA924763	976 AI176596	179 AA859938			1051 AI178968	490 AF034218	230 AA892027	844 Al169166	1015 AI177489	980 A1176648	789 AI112365	825 A145081		1070 AI179857
#401 m 4	omparison Code	220E7 D	22337 R	22301 E	23000 H	23005 F.P		23013.1	2303011	23032 K	23033 G			23043 N	23044 A H	23047 H	23075 A	23077 H	23082 A	23000	23106 O B	5	23120 C,D

Document Number 1650775	The Unione Cluster Title	ESTS	ESTs	ESTs	Rattus norvegicus I-kappa-B-beta	mRNA, complete cds	ESTs, Weakly similar to C43H8.1	[C.elegans]	ESTs, Highly similar to CRIP_MOUSE	CYSTEINE-RICH INTESTINAL	PROTEIN [R.norvegicus]	ESTs	Rattus norvegicus evectin-1 (EVT1)	mRNA, complete cds	ESTs	Rattus norvegicus mRNA for 3'(2'),5'-	bisphosphate nucleotidase	ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to Bop1	[M.musculus]	ESTs	ESTs	R.norvegicus mRNA for prolyl 4-	hydroxylase alpha subunit
	Woown Cana Nama				HMm:nuclear factor of kappa light chain Rattus norvegicus I-kappa-B-beta	gene enhancer in B-cells inhibitor, beta mRNA, complete cds											HMm:bisphosphate 3'-nucleotidase 1									HMm:procollagen-proline, 2- oxoglutarate 4-dioxygenase (proline 4-	hydroxylase), alpha 1 polypeptide
		Lamada															Sulfur metabolism									Arginine and proline	metabolism
	ep ep	1172 A1232266	561 Al013011	1076 AI180040		960 AI176319		850 AI169317			312 AA925057	1141 AI230981		819 AI144586	974 AI176554		1319 AJ000347	1229 AI234038	1266 AI236146	138 AA851803	1066 AI179570		856 AI169617	314 AA925145	989 A1176839		1516 X78949
TARLE	1 5	10 Code	23125 B, C	23139 H		23160 C.L		23170 E			23173	23182 F.N		2318310	23184 C	2	23220 0	23229 C	23230 A.H.N	23243 E	23245 0	3	23260 C.D	23261 A.C.D	23299 C		23302 I,N

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Document Number 1650775	Unigene Cluster Title		R.norvegicus mRNA for prolyl 4-	hydroxylase alpha subunit		Rattus norvegicus aiar mRNA for	androgen-inducible aldehyde reductase,	S	Rattus norvegicus aiar mRNA for	androgen-inducible aldehyde reductase,	S	ESTs, Weakly similar to TCPA_RAT T-	COMPLEX PROTEIN 1, ALPHA	SUBUNIT [R.norvegicus]		ESTs, Highly similar to Mlark	[6	Rattus nonvegicus double-stranded RNA	binding protein p74 mRNA, complete cds	Ras homolog enriched in brain		ESTs, Weakly similar to TCPA_RAT T-	COMPLEX PROTEIN 1, ALPHA	SUBUNIT [R.norvegicus]	ESTs, Highly similar to KIAA0601 protein			ESTs, Highly similar to F25965 1	
			R.norvegicu	hydroxylase	ESTs	Rattus norve	androgen-in	complete cds	Rattus norve	androgen-in	complete cds	ESTs, Weak	COMPLEX	SUBUNIT [F	ESTs	ESTs, Highl	[M.musculus]	Raffils norve	binding prot	Ras homolo	ESTs	ESTs, Weak	COMPLEX	SUBUNIT [F	ESTs, Highl	[H.sapiens]	ESTs	ESTs, High	
	Known Gene Name	HMm:procollagen-proline, 2-	oxoglutarate 4-dioxygenase (proline 4-	hydroxylase), alpha 1 polypeptide							4									Ras homolog enriched in brain									
	Pathways		Arginine and proline	metabolism																									
	GenBank			1153 AI231310	239 AA892425			247 AA892821			247 AA892821			181 AA859980	928 AI172405		1210 AI233457		520 AI009096	1616 NM 013216	141 AA851961			927 AI172328		1112 AI229502	661 AI071166		_
	Nucleotide Sequence			1153	239			247			247			181	928		1210		520	1616	141			927		1112	661		_
,	GEGC Comparison			Ш	E,R			А			⋖			Ш	A		<u></u>		0	0	A			D,G		ပ	A,O		
TABLE	GLGC			23304 E	23315 E,R			23321			23322 A			23324 E	23325 A		23331		23337 E.O	23362 0	23380 A			23390 D,G		23435 C	23437 A,O		

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Document Number 1650775	n n n n n n n n n n n n n n n n n n n	Flavin-containing monooxygenase 1	ESTs	ESTs	acidic calponin	ESTs	EST	ESTs	ESTs	ESTs, Highly similar to S23B_HUMAN PROTEIN TRANSPORT PROTEIN	SEC23 HOMOLOG ISOFORM B	[H.sapiens]	Ornitine decarboxylase		Ornitine decarboxylase	ESTs	ESTs, Weakly similar to NDKA_RAT	NUCLEOSIDE DIPHOSPHATE KINASE	A [K.norvegicus]	ESTs	ESTs	ESTs
			Ш	Ш	ä	ŭ	Ш	Ü	Ü	<u> </u>	S	븨	0		0	Ш	Ш	Z ·	4	Ш	<u>Ü</u>	쁴
	Known Gene Name	Flavin-containing monooxygenase 1			acidic calponin								Ornitine decarboxylase		Ornitine decarboxylase							
	Pathways												Arginine and proline metabolism, Urea cycle and metabolism of amino groups	Arginine and proline	metabolism, Urea cycle and metabolism of amino groups							
	GenBank Acc ID	1571 NM 012792	315 AA925167	987 AI176828	1681 NM_019359	AI170967	393 AA955249	183 AA860010	1697 NM 022294			1063 AI179498	1552 NM_012615		1552 NM 012615	394 AA955443			400 AA956170	1042 AI178746	392 AA955071	977 AI176598
	Nucleotide Sequence ID	1571	315 /	/ 186	1681	888	393 /	183	1697			1063	1552		1552	394			400	1042	392	977
	GLGC Comparison Sequence ID Code ID	D,F	3	3,0	O,N,F	フ	4	4,S	4			ı	Ш. -{r [†]		ď	M.P			∀	ſ	A,B	ſ
TABLE 1) 019	23445 A,D,F	23448 B	23449 B,Q	23491 H,N,O	23494 N	23499 A	23500 A,S	23511 A			23515	23522 A.F		23523 A	23555 M.P			23558 A	23567	23584 A,B	23587

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Document Number 1650775	ne Name Lunigene Cluster Title	Rattus norvegicus microtubule-	associated proteins 1A and 1B light	chain 3 subunit mRNA, complete cds	Rattus norvegicus microtubule-	associated proteins 1A and 1B light	chain 3 subunit mRNA, complete cds	ESTs	ESTs	ESTs, Moderately similar to	AF151890_1 CGI-132 protein	[H.sapiens]	ESTs		ESTs		gene 3 B-cell translocation gene 3	, 3-oxo acyl-	oxisomal CoA thiolase A, peroxisomal	sporting beta 1 ATPase Na+/K+ transporting beta 1	polypeptide	nsporting beta 1 ATPase Na+/K+ transporting beta 1	polypeptide	nsporting beta 1 ATPase Na+/K+ transporting beta 1	polypeptide	ESTs, Highly similar to Lsm5 protein	[H.sapiens]	ESTs	ESTs	EST
1	Pathways Known Gene Name													Sialoprotein (osteopontin)		B-cell translocation gene 3	B-cell translocation gene 3	Acetyl-CoA acyltrans	CoA thiolase A, peroxisomal	ATPase Na+/K+ transporting beta 1	polypeptide	ATPase Na+/K+ transporting beta 1	polypeptide	ATPase Na+/K+ transporting beta 1	polypeptide					
	Nucleotide Sequence GenBank ID Acc ID Pal			1714 NM 022867			1201 AI233190	880 AI170751	395 AA955540			628 AI045624	706 AI101130	1582 NM_012881	616 AI044533	1674 NM_019290	1674 NM_019290		1532 NM_012489		1603 NM_013113		1135 AI230614		1603 NM 013113		404 AA956431	1295 AI237207	412 AA957410	405 AA956723
TABLE 1	GLGC Comparison Sequ			23606 H,N			23608 E	23612 A	23626 N			23627 S	23633 A	23651	23656 R	23678 C	23679 A,C,D,F		23698 E		23709 H,K		23710 H		23711 H		23762 R	23767 A	23843 E,R	23847 B

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Bocument Number 1650775	enter de la companya	Unigene Cluster Title	R.norvegicus (Sprague Dawley)	ribosomal protein L13 mRNA	ESTs	Early growth response 1	Early growth response 1	Early growth response 1											Rat microsomal aldehyde	dehydrogenase mRNA, complete cds	ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to Bcl-2-interacting	protein beclin [H.sapiens]	ESTs	fumarylacetoacetate hydrolase	ESTs	ESTs	ESTs
		Known Gene Name 🛪 🖈				Early growth response 1	Early growth response 1	Early growth response 1											aldehyde dehydrogenase 4, liver	microsomal (class 3)								fumarylacetoacetate hydrolase			
	30 22	Pathways							Arginine and proline	metabolism, Ascorbate and	aldarate metabolism, Bile	acid biosynthesis, Butanoate	metabolism, Fatty acid	metabolism, Glycerolipid	metabolism, Histidine	metabolism, Lysine	degradation, Phenylalanine	metabolism, Propanoate	metabolism, Pyruvate	metabolism								Tyrosine metabolism			
	GenBank	Accilia		1514 X78327	1287 AI236773	1543 NM_012551	1543 NM 012551	1543 NM_012551												1422 M73714	866 AI170007	AA892520	241 AA892520	406 AA956864		409 AA957071	1103 AI229178	1640 NM_017181	1496 X51615	1072 AI179953	411 AA957335
	Nucleotide Sequence			1514	1287	1543	1543	1543												1422	866	241	241	406		409	1103	1640	1496	1072	411
-	Comparison	Code		G,I	B,C	L	ш.	L												_ ✓	Ш	_	Σ	B		Ш	A S	A,D	0	B,Q	O,M
TABLE 1	36 GC	ID.		23854 G,	23855 B,C	23868	23869	23872 F												23884 A	23885	23888	23889 M	23890 B		23945 F	23955 A	23961 A,D	23987 0	23989 B,Q	24012 M,O

Comment Number 1650775	Unigene Cluster Title	Rattus norvegicus p55CDC mRNA,	complete cds	ESTs, Highly similar to CGI-10 protein	[H.sapiens]	EST	ESTs	ESTs	ESTs	ESTs, Weakly similar to hypothetical	protein [H.sapiens]	ESTs	ESTs	ESTs	Rattus norvegicus tyrosine phosphatase	(PRL-1) mRNA, complete cds	ESTs	ESTs, Weakly similar to A1AT_RAT	ALPHA-1-ANTIPROTEINASE	PRECURSOR [R.figliveglcus]	Rattus norvegicus NADPH-dependent	thioredoxin reductase (TRR1) mRNA,	complete cds	Rattus norvegicus NADPH-dependent	thioredoxin reductase (TRR1) mRNA,	complete cds	ESTs	ESTs
	Known Gene Name															protein tyrosine phosphatase 4a1												
	Pathways																											
	Nucleotide Sequence GenBank ID Acc ID		496 AF052695		1010 AI177341	414 AA957452	935 A1175423	514 AI008773	415 AA957708		859 AI169668	150 AA858588	847 AI169279	555 AI012356		1395 L27843	871 AI170385			30 AA800318	-		1469 U63923		<u>-</u>	213 AA891286	967 AI176473	44 AA817726
TABLE 1	GLGC Comparison ID Code		24024 Q		24049 G	24051 L	24079 H	24112 0	24126 R		24146 E	24161 E	24162 A	24200 N		24219 A	24227 L			24228 M			24234 J			24235 A.D.J	24236 C,L	24237 F,M

Pathways Known Gene Name ESTS Highly similar to cell cycle processe Subtilisin - like endoprotease Subtilisin - like endoprotease ESTS Rattus norvegicus nucleolar Phosphoprotein of 140kD, Nopp14	TABLE 1.	The Manual Property of the Control o					
ESTs, Highly similar to cell cycle progresse Subtilisin - like endoprotease Subtilisin - like endoprotease ESTs Rattus norvegicus nucleolar phosphoprotein of 140kD, Nopp14(mRNA, complete cds ESTs, Highly similar to galactokina [M.musculus] ESTs ESTs, Highly similar to steroidogen acute regulatory protein [R.norvegicus] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	Comparison Sequence GenBank Code ID Acc ID	Sequence ID	GenBank Acc (D		S : Pathways	iKnown Gene Name	Unigene Cluster Title
Subtilisin - like endoprotease Subtilisin - like endoprotease ESTs Rattus norvegicus nucleolar phosphoprotein of 140kD, Nopp14(mRNA, complete cds ESTs, Highly similar to galactokinas ESTs, Highly similar to steroidogen acute regulatory protein [R.norvegicus] ESTs, Moderately similar to GTM1 GLUTATHIONE S-TRANSFERASE [R.norvegicus] EST ESTS, Highly similar to AF114169_ nucleotide-binding protein short for [M.musculus] ESTS, Highly similar to AF114169_ nucleotide-binding protein short for [M.musculus] ESTS, Moderately similar to nucleo protein p40 [H.sapiens] ESTS ESTS, Moderately similar to nucleo protein p40 [H.sapiens] ESTS ESTS ESTS Rat mannose-binding protein C (liv mRNA, complete cds Rat matrin F/G mRNA, complete cds							ESTs, Highly similar to cell cycle protein
Subtilisin - like endoprotease ESTS Rattus norvegicus nucleolar phosphoprotein of 140kD, Nopp14(mRNA, complete cds		419 AA963703	AA963703			11	p38-2G4 homolog [H.sapiens]
ESTS Rattus norvegicus nucleolar phosphoprotein of 140kD, Nopp14f mRNA, complete cds ESTS, Highly similar to galactokina [M.musculus] ESTS, Highly similar to steroidogen acute regulatory protein [R.norvegicus] ESTS ESTS, Moderately similar to GTM1 GLUTATHIONE S-TRANSFERASE [R.norvegicus] ESTS ESTS, Highly similar to AF114169_nucleotide-binding protein short for [M.musculus] ESTS, Highly similar to AF114169_nucleotide-binding protein short for [M.musculus] ESTS, Moderately similar to nucleo protein p40 [H.sapiens] ESTS, Moderately similar to nucleo protein p40 [H.sapiens] ESTS ESTS Rat mannose-binding protein C (livent MRNA, complete cd	24264 A 1593 NM_012999	1593 NM_012999	NM_012999			Subtilisin - like endoprotease	Subtilisin - like endoprotease
Rattus norvegicus nucleolar phosphoprotein of 140kD, Nopp14t mRNA, complete cds ESTs, Highly similar to galactokina [M.musculus] ESTs, Highly similar to steroidogen acute regulatory protein [R.norvegicus] ESTs ESTs, Moderately similar to GTM1 GLUTATHIONE S-TRANSFERASE [R.norvegicus] EST	24268 E 924 A1172281	924 AI172281	AI172281				ESTs
ESTS, Highly similar to galactokina Galactokinase ESTS, Highly similar to galactokina ESTS, Highly similar to steroidogen acute regulatory protein [R.norvegia ESTS, Moderately similar to GTM1 GLUTATHIONE S-TRANSFERASE [R.norvegicus] EST EST ESTS, Highly similar to AF114169 nucleotide-binding protein short for [M.musculus] ESTS, Moderately similar to nucleo protein p40 [H.sapiens] ESTS, Moderately similar to nucleo protein p40 [H.sapiens] ESTS ESTS Rat mannose-binding protein C (liventally complete or Rat mannose-							Rattus norvegicus nucleolar
ESTS, Highly similar to galactokina Galactokinase [M.musculus] ESTS, Highly similar to steroidogen acute regulatory protein [R.norvegie ESTs] ESTS, Moderately similar to GTM1 GLUTATHIONE S-TRANSFERASE [R.norvegicus] EST ESTS, Highly similar to AF114169] nucleotide-binding protein short for [M.musculus] ESTS, Highly similar to nucleo protein p40 [H.sapiens] ESTS ESTS ESTS Rat mannose-binding protein C (liven MRNA, complete or Rat matrin F/G mRNA, complete or	24284 A 1715 NM 022869	1715 NM 022869	NM 022869				mRNA, complete cds
Galactokinase ESTs, Highly similar to steroidogen acute regulatory protein [R.norvegie ESTs		***************************************					ESTs, Highly similar to galactokinase
Highly similar to steroidogen regulatory protein [R.norvegia Moderately similar to GTM1-ATHIONE S-TRANSFERASE vegicus] Highly similar to AF114169—stude-binding protein short for sculus] Highly similar to AF114169—stude-binding protein short for sculus] Moderately similar to nucleo n p40 [H.sapiens] annose-binding protein C (livannose-binding protein C (livannose	24289 B,Q 399 AA955986 Ga			Ga	lactose metabolism	Galactokinase	[M.musculus]
regulatory protein [R.norvegi Moderately similar to GTM1 ATHIONE S-TRANSFERASE vegicus] Highly similar to AF114169 pitde-binding protein short for sculus] Highly similar to AF114169 pitde-binding protein short for sculus] Moderately similar to nucleo n p40 [H.sapiens] annose-binding protein C (livannose-binding protein C (livannose-b						4.	ESTs, Highly similar to steroidogenic
Moderately similar to GTM1-vegicus] Highly similar to AF114169-stude-binding protein short for sculus] Highly similar to AF114169-stude-binding protein short for sculus] Moderately similar to nucleon p40 [H.sapiens] annose-binding protein C (livannose-binding protein C (livann	24296 E 1360 H32867	1360 H32867	H32867				acute regulatory protein [R.norvegicus]
Moderately similar to GTM1- ATHIONE S-TRANSFERASE vegicus] Highly similar to AF114169 titde-binding protein short for sculus] Highly similar to AF114169 hide-binding protein short for sculus] Moderately similar to nucleo n p40 [H.sapiens] annose-binding protein C (livannose-binding protein C (livannose-bi	24321 A,D,G 1178 AI232340	1178 AI232340	AI232340				
R.norvegicus EST							ESTs, Moderately similar to GTM1_RAT
EST ESTS, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus] ESTS, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus] ESTS, Moderately similar to nucleolar protein p40 [H.sapiens] ESTS ESTS ESTS Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds							GLUTATHIONE S-TRANSFERASE YB1
ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus] ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus] ESTs, Moderately similar to nucleolar protein p40 [H.sapiens] ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds	24323 P 763 AI104798	763 AI104798	AI104798				[K.norvegicus]
ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus] ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus] ESTs, Moderately similar to nucleolar protein p40 [H.sapiens] ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds	R 401 AA956247	401 AA956247	AA956247				EST
Inucleotide-binding protein short form [M.musculus] ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus] ESTs, Moderately similar to nucleolar protein p40 [H.sapiens] ESTs ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds							ESTs, Highly similar to AF114169_1
ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus] ESTs, Moderately similar to nucleolar protein p40 [H.sapiens] ESTs ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds	1080 A1180302	1080 4180392	A1180392				nucleotide-binding protein short form [M.musculus]
iM.musculus] ESTs, Moderately similar to nucleolar protein p40 [H.sapiens] ESTs ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds							ESTs, Highly similar to AF114169_1
[M.musculus] ESTs, Moderately similar to nucleolar protein p40 [H.sapiens] ESTs ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds							nucleotide-binding protein short form
ESTs, Moderately similar to nucleolar protein p40 [H.sapiens] ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds	24369 R 346 AA944011	346 AA944011	AA944011				[M.musculus]
protein p40 [H.sapiens] ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds							ESTs, Moderately similar to nucleolar
ESTs ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds	24375 A,D 766 Al104979	766 AI104979	AI104979				protein p40 [H.sapiens]
ESTs Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds	S 403 AA956301	403 AA956301	AA956301				ESTs
Rat mannose-binding protein C (liver) mRNA, complete cds Rat matrin F/G mRNA, complete cds	24388 C.D.I.R 1286 AI236772	1286 AI236772	AI236772				ESTs
mRNA, complete cds Rat matrin F/G mRNA, complete cds				L			Rat mannose-binding protein C (liver)
Rat matrin F/G mRNA, complete cds	24434 A 1710 NM_022704	1710 NM_022704	NM_022704				mRNA, complete cds
	24442 O 1708 NM_022667	1708 NM_022667	NM_022667				Rat matrin F/G mRNA, complete cds

TARIE 1	The state of the s			h a ja vii de saara ja vii saara		Document Number 1650775
0) 00/19	nparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known!Gene Name	Unigene Cluster Title
24453 F	吐	1560	1560 NM_012690		P-glycoprotein 3/ multidrug resistance 2,P-glycoprotein/multidrug resistance 1	P-glycoprotein 3/ multidrug resistance 2
24458 A	A	1711	1711 NM_022706			Rat metabotropic glutamate receptor (GLUR4) mRNA, complete cds
24501	۵	1167	1167 AI232006			Rattus norvegicus translation elongation factor 1-delta subunit mRNA, partial cds
24508	Ш	1416	1416 M34643			Rat neurotrophin-3 (HDNF/NT-3) mRNA, complete cds
24577	⋖	1498	1498 X55153			ESTs, Highly similar to RLA2_RAT 60S ACIDIC RIBOSOMAL PROTEIN P2 [R.norvegicus]
24589 E,P	டி	1558	1558 NM_012674		Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic	Serine protease inhibitor, kanzal type 1/ Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic
24597 C	O.	1625	1625 NM_017040		Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
24645 A	Ą	1484	1484 V01225	Starch and sucrose metabolism	HMm:amylase 2, pancreatic	Rat pancreatic amylase mRNA, partial coding sequence
24651	۵	1426	1426 M83678			Sprague-Dawley (clone LRB10) RAB13 mRNA, 3'end
24654 E	Ш	100	100 AA819333			Sprague-Dawley (clone LRB2) RAB16 mRNA, complete cds
24670 G	9	1642	1642 NM_017189		asialoglycoprotein receptor 2	asialoglycoprotein receptor 2
24707 E,O	, E,O	1561	1561 NM_012693	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450 IIA2	Cytochrome P450 IIA2
24710 C	C	1430	1430 M98820	interact6-1	Interleukin 1 beta	Rat interleukin 1-beta mRNA, complete cds

Document Number 1650775	Unigene Gluster Title	ESTs	Plasma kallikrein	Solute carrier family 10 (sodium/bile acid	cotransporter family), member 1			Rat serine dehydratase (SDH2) mRNA,	complete cds	Rat N-hydroxy-2-acetylaminofluorene	(ST1C1) mRNA, complete cds	Rat N-hydroxy-2-acetylaminofluorene	(ST1C1) mRNA, complete cds	Rat thyroxine-binding globulin (TBG)	mRNA, 3' end					Rat liver UDP-glucuronosyltransferase,	phenobarbital-inducible form mRNA,	complete cds	carbonic anhydrase 5							
	Knowh Gene Name		Plasma kallikrein	Solute carrier family 10 (sodium/bile	acid cotransporter family), member 1				HHs:serine dehydratase		sulfotransferase, phenol preferring 2		sulfotransferase, phenol preferring 2							Hsp:UDP-	GLUCURONOSYLTRANSFERASE	2B1 PRECURSOR, MICROSOMAL	carbonic anhydrase 5							
	Pathways					Cysteine metabolism,	Glycine, serine and	threonine metabolism,	Oxidative phosphorylation		Sulfur metabolism		Sulfur metabolism			Androad and actrodon	metabolism, Pentose and	glucuronate	interconversions, Porphyrin	and chlorophyll metabolism,	Starch and sucrose	metabolism	Nitrogen metabolism							
	GenBank Acc ID	99 AA819306	1564 NM 012725	-	1626 NM_017047				1375 J03863		1391 L22339		L22339		1421 M63991							1403 M13506	1677 NM 019293	1353 E03229	1390 L22190	L36460	1398 M11251	1402 M13234	1440 S82820	1453 U20643
	Nucleotide Sequence In		1564		1626				1375		1391		1391		1421							1403	1677	1353	1390	13961	1398	1402	1440	1453
	GLGC Comparison	lo	9		A,G				<u>LL</u>		я Б		<u> </u>		۵					2		K.S	3A	1 F	25052 A.F.M.P	1 A	Z K	3 K,L	25069 F,G	7 Q
TABLEA	0979 0979	₩ 🕶	24722 G		24771 A,G				24779		24810 F.G		24811 G		24826 P							24860 K.S	24883 A	25024 F	25052	25054 A	25055 K	25056 K,L	25069	25077 Q

Document Number 1650775	Unigene Clüster Title																											
	Known Gene Name				-			HSp:MEMBRANE COPPER AMINE	UNIDAGE		insulin receptor substrate 2															HSp:GLUTATHIONE S- TRANSFERASF YC.1		
	Pathways	Arginine and proline metabolism, Glycine, serine	and threonine	metabolism, Histidine	metabolism,Phenylalanine	metabolism,Tryptophan	metabolism, Tyrosine	metabolism,beta-Alanine	Hetabolishi																	Glutathione metaholism		
	GenBank Acc 10							00000711	0/2032	AA108277	495 AF050159	1689 NM_021754	501 AF079873	1321 AJ011607	1328 D13623	1339 D42148	1347 D87991	1387 L16995	1394 L26292	1401 M12822	1408 M18527	1409 M18528	1410 M18529	1411 M18531	1432 S46785	1437 872505	1441 S85184	1466 U58466
	Nucleotide n Sequence ID							7 7 7 2	C/4/	-	495	1689	501	1321	1328	1339	1347	1387	1394	1401	1408	1409	1410	1411	1432	1437	1441	1466
LE1	GLGC Comparison ID Code								Z0002 F	1 86 J	25183 K	98 J	25203 E	25246 M	25257 C,I	25290 M,O	13	25370 B,Q	25379 Q	25397 E	25409 E	25410 E	25411 E	25413 E	25480 A,G	טבבטג ם	25567 A.J	25615 E
TABLE	GLG D							Č	7007	25098	2518	25198 J	252	252,	252	252	25313	253	253	253	254	254	254	254	254	25.5	255	256

Document Number 1650775																															
		Known Gene Name									ribosomal protein L8																				
		Pathways Pathways																													
	Nucleotide SenBank		1470 U64705	1470 064705	1476 U75405	1479 U77931	1493 X14181	1502 X58465	1504 X59375	1506 X59608	1508 X62145	1510 X62660	1518 X81448	1520 X94769	1523 Y08355	1352 E02315	1696 NM_022268	1305 AI638998	1309 AI639101	1313 AI639167	1314 AI639281	291 AA901152	441 AA997009	511 AI008396	532 AI009950	563 AI013387	576 AI028938	688 AI072578	1082 AI227562	1134 AI230577	1242 AI234927
TABLE 1	GLGC Comparison	Code	25618 M	25619 M	25632 G	25644 E	25675 A	25702 A	25705 H	25706 L	25718 1,0	25725 K	25747 A,F	25768 Q	25777 E	25802 E,I	25814 H	25852 L	25892 G	25907 J	25938 B	26088 E	26109 S	26123 D	26133 M	26147 E	26152 N	26190 E,R	26280 Q	26288 E	26320 M

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FABLE 1	25.0	38E	26369 C.D
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FABLE 2 Comparison	Document Number 1650775
Comparison	Comparison Code
General Toxicity: Amitryptiline, ANIT, APAP,	
CCI4, Diclofenac, Indomethacin, Valproate,	
Untreated Rats, Various Vehicles, WY-14643,	
Cyproterone Acetate, and Estradiol	A
Hepatitis-inducing and NSAIDS: Diclofenac and	
Indomethacin	В
Necrosis and Fatty Liver: Carbon Tetrachloride	
and Valproate	С
Necrosis With and Without Fatty Liver: Carbon	_
Tetrachloride, Valproate, and Acetaminophen	D
Protein Adduct Formers: Valproate and	E
Diclofenac	<u> </u>
ANIT	F
Late Acetaminophen	G
Early Acetaminophen	H
Late Carbon Tetrachloride	1
Early Carbon Tetrachloride	J
Late Cyproterone Acetate	K
Early Cyproterone Acetate	L
Late Diclofenac	M
Early Diclofenac	N
Estradiol 4	0
Late Indomethacin	P
Early Indomethacin	Q
Valproate	R
WY-14643	S

TABLE 3A: (General Toxic	ity		Document	Number 1650775
VINE WAR AND LOCAL TO A DESCRIPTION OF THE PERSON OF THE P	Tox Mean		LDA Score	\$2566\$2525555755577 × > 1/25/315/325755 / 1588455 (\ \$44.5).	Non Tox Stdev
21471	30.43	93.54	75	-42.67	24.83
13203	35.33	61.64	74	-31.14	29.79
19909	22.08	33.51	73	-15.41	29.38
4553	13.83	18.08	72	1.43	6.49
15301	124.27	140.5	77	5.51	36.16
20456	42.5	31.85	70	7.46	20.45
23679	57.12	66.55	72	8.07	7.49
14693	37.57	38.27	72	9.49	11.63
12471	26.73	25.33	73	9.55	21.73
923	60.74	80.74	71	9.6	6.57
15647	49.51	40.73	72	10.9	23.58
6322	45.84	55.48	70	12.42	10.76
16314	48.7	48.51	70	12.45	16.75
25052	90.08	154.89	70	14.05	18.5
2164	57.65	53.74	73	14.96	17.31
16006	58.93	36.27	80	15.18	19.39
25054	45.65	42.59	72	15.37	40.01
	4.65	23.5	70	15.8	61.49
6410		35.28	70	16.65	11.6
23500	39.03		75	17.24	10.59
16312	39.06	24.35	74	17.7	10.31
19843	2.55	18.74	71	20.43	22.52
14996	58.1	47.71 45.9	70	21.59	14.6
16085	60.79		70	23.22	18.41
17982	49.3	27.48	71	23.54	10.28
6226	46.81	36.97	-		25.4
9326	6.05	16.52	70	24.18	26.9
15055	-7.1	34.32	70	26.37	19.43
351	94.58	92.7	71		14.06
1126	48.74	21.68	72	26.96	26.92
20161	87.17	88.37	76	27.44	35.81
8766	-14.3	48.76	75	27.97	16
23511	12.84	20.12	72	29.05	16.66
5461	77.51	74.15	71	29.28	80.65
12216	-22.58	61.28	71	29.83	
5384	100.6	91.07	76	30.03	29.52
18389	43.98	46.66	74	31.53	26.82
21695	45.44	55.44	72	31.53	16.62
11357	17.28	18.76	73	31.76	16.7
14424	567.82	812.48	70	32.4	34.02
9331	60.44	27.33	70	33.81	15.06
23767	23.85	17.49	71	34.2	50.3
15862	62.08	31.33	71	34.72	12.31
20449	117.61	143.09	71	35.82	9.2
10248	68.54	26.33	77	36.88	16.24

TABLE 3A:	General Tox	icity		Document	Number 1650775
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
23082	23.23	17.75	71	37.04	12.65
9425	17.36	27.44	71	37.87	17.12
16730	73.58	39.38	73	39.09	20.24
9583	161.94	162.1	73 ·	39.37	25.85
11563	71.92	56.8	70	39.98	27.02
352	130.52	119.67	76	40.04	18.99
6604	24.19	16.7	74	41.3	15.53
7243	91.87	50.42	74	41.4	14.59
17709	71.49	47.04	70	41.77	28.89
1583	62.93	26.33	71	41.81	9.01
761	28.63	19.45	70	43.38	21.32
3849	81.84	39.76	71	43.61	16.59
24284	65.8	20.86	74	45.29	13.2
3207	25.59	109.41	70	45.31	54.06
21707	108.81	66.66	72	45.32	39.4
17589	85.64	50.71	71	46.93	27.53
22212	112.59	77.44	70	47.96	21.25
5175	72.78	115.19	71	48.48	31.56
7299	220.49	225.32	77	49.33	34.75
19678	3.58	46.62	75	49.59	34.93
21088	58.85	18.82	72	51.63	11.12
15892	152	118.78	75	52.52	42.58
14353	84.25	29.24	74	53.47	12.39
11527	119.25	79.46	70	54.98	27.79
13749	38.3	29.23	73	55.43	20.89
4281	38.95	21.16	70	57.15	17.8
353	194.24	177.12	76	57.46	26.37
14206	41.14	16.67	73	57.71	14.34
16080	207.65	183.99	77	58.82	28.68
6682	53.78	37.44	70	59.02	19.46
825	42.12	20.91	71	59.35	17.09
7918	90.4	45.57	71	60.65	23.06
21150	138.34	101.42	71	64.19	46.67
7531	57.13	26.96	70	64.99	18.47
22487	81.97	69.8	71	66.94	27.76
24264	112.04	51.05	72	67.41	29.12
22077	46.19	26.57	70	67.77	24.16
21209	174.43	157.48	73	70.46	46.49
20772	102.74	37.31	72	70.49	15.59
8600	33.46	36.07	72	71.84	38.68
9826	49.36	28.75	70	72	22.77
17688	108.65	39.15	70	72.62	19.69
6640	40.46	39.18	74	73.64	29.52
3074	75.98	91.66	70	73.84	44.71

TABLE 3A:	General Toxi	city		Document	Number 1650775
				Non Tox Mean	
4473	54.98	25.48	70	74.37	21.06
354	227.5	203.23	77	74.89	23.89
23522	107.75	42.24	73	74.91	18.29
15299	176.87	143.39	75	75.35	20.66
13166	145.19	92.31	71	75.39	33.67
7936	59.06	21.73	70	76.33	18.71
17819	57.46	25.12	71	76.84	20.15
17908	191.58	159.91	71	77.06	30.42
7681	125.85	57.35	71	77.88	39.68
23633	66.31	40.72	70	78.12	28.98
19508	49.65	31.49	70	78.53	32.19
9541	166.47	123.33	72	79.59	34.68
16446	58.49	21.61	71	80.2	20.86
17377	119.83	80.06	72	82.65	37.63
20801	136.04	60.94	71	83	38.58
7352	164.48	94.53	70	83.91	38.34
2901	63.21	31.06	71	84.9	24.78
15156	85.12	43.67	71	85.31	23.45
22877	140.94	62.91	71	85.66	25.88
15207	112.17	89.27	73	85.8	32.15
	 	 		86.7	25.5
9627	65.98	37.05	73		27.99
4017	71.08	40.29	70	86.72	
4944	252.32	217.46	76	86.84	38.34
3073	78.22	126.03	72	87.19	58.64
5046	99.33	75.05	70	91.34	37.3
3713	66.05	38.37	71	91.52	27.81
11576	56.54	27.2	75	92.19	28.07
1246	57.52	28.55	70	92.34	25.09
15382	699.61	884.63	73	92.89	30.78
18109	105.09	108.04	71	93.58	44.98
18906	66.76	34.6	72	93.87	22.06
16324	65.53	39.09	72	94.25	27.97
7903	31.76	35.55	72	94.94	65.97
7063	179.3	93.83	74	95.16	22.48
9053	60.23	42.49	72	97.12	25.77
5813	67.41	28.11	70	97.48	35.73
9245	39.62	45.11	73	97.55	55.74
16081	293.48	225.5	78	97.81	34.89
19085	146.97	54.5	71	98.39	27.86
3189	48.18	30.77	70	99.15	55.31
12655	74.53	78.23	70	99.85	45.15
5219	54.76	44.93	70	100.79	47.29
7062	157.19	68.98	70	101.14	24.11
6820	132.9	40.9	71	101.15	18.57

TABLE 3A:	General Tox	icity		Documen	t Number 1650775
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
21025	52.78	49.73	75	102	38.88
14746	72.12	42.89	70	102.6	35.3
11745	127.84	29.61	71	102.7	19.78
20035	330.62	323.46	73	105.65	47.24
12587	72.78	43.64	72	105.95	35.48
2372	89.09	42.56	70	107.07	30.91
2383	87.59	39.36	72	108.56	32.43
2532	28.55	57.57	72	109.2	73.94
11959	91.5	26.27	70	109.84	20.36
24375	200.33	108.66	72	110.42	32.85
15884	135.81	86.11	70	111.91	36.88
2576	81.51	44.81	71	112.47	36.08
23955	98.48	60.26	72	113.59	36.89
5008	152.54	61.16	71	113.65	24.98
20891	174.25	85.84	72	114.45	35.06
18390	78.44	44.36	70	116.93	42.8
1844	172.33	73.68	70	117.06	23.94
17591	177.66	76.44	70	119.35	26.88
22038	178.88	77.12	70	119.93	32.92
20874	102.83	26.99	76	120.76	19.57
	 	107.09	73	120.76	50.32
17844	225.91	49.49	73	124.21	42.81
11691	80.29		72	124.7	32.65
19086	192.42	71.46	75	125.88	34.64
14937	93.31	50.67			74
20513	76.12	59.17	72	127.29	44.99
6037	90.3	39.56	73	127.31	100.98
12332	24.75	72.13	73	128.95	
17335	99.84	36.82	73	129.97	30.57
134	71.14	58.38	77	133.41	39.47
7784	109.76	36.32	70	134.08	25.84
25567	222.63	133.25	70	134.17	40.36
4951	296.48	152.65	74	135.21	102.87
13351	87.72	56.78	76	135.45	45.49
22432	207.69	93.56	71	137.45	35.3
3075	134.78	146.57	74	138.67	65.46
16134	88.41	44.61	74	139.59	36.27
18660	99.04	62.72	74	141.07	60.13
17225	208.62	72.16	71	141.32	36.37
10509	91.25	50	70	142.42	48.95
6190	108.44	39.25	71	142.68	30.93
17393	216.6	101.01	70	144.48	27.96
22197	295.18	157.65	75	144.6	54.77
19952	98.31	43.39	75	145.63	36.13
1690	206.44	90.45	70	147.21	36.46

TABLE 3A:	General Toxi	city		Document	Number 1650775
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
23044	188.12	53.18	74	148	23.7
22931	50.06	64.25	72	148.05	101.64
14776	103.46	45.74	74	148.29	40.54
14051	218.89	97.53	70	149.85	36.11
22569	103.93	53.65	76	150.14	42.57
11403	485.69	353.08	74	150.23	94.34
13762	105.01	72.99	71	151.26	47.6
14074	72.32	60.1	74	153.35	74.91
18960	120.13	59.4	71	156.6	44.43
20889	193.77	86.18	70	156.83	37.64
4084	127.09	64.08	71	158.37	49.57
18854	124.79	56.31	70	158.52	38.36
20735	294.63	147.51	80	164.19	33.2
14181	117.28	41.72	73	165.97	41.05
24883	122.66	51.37	75	165.99	38.66
15933	192.2	65.93	70	166.13	35.32
18792	112.37	55.57	73	167.2	48.33
10544	240.01	60.23	77	167.22	32.41
14208	98.76	46.96	77	167.76	48.04
20734	292.65	126.84	78	169.42	39.52
		131.16	76	170.46	50.64
17334 22457	283.45 319.78	159.2	71		83.07
	127.23	34.44	75	170.89 172	37.41
21978		33.78	75	173.08	29.79
15300	138.87 301.38	143.25	73	174	53.02
16364		72.42	74	<u> </u>	56.68
	109.25		74	174.33	39.95
8829	280.85 71.78	107.19 95.85	73	174.35 174.52	94.52
1007				174.54	46.87
17154	130.76 237.49	76.39 69.3	77	174.79	36.28
		42.8	72	175.56	60.84
6473 2335	107.85 121.97	52.51	71	175.91	56.34
		92.4	75	181.36	63.89
12450	90.03	131.83	75		86.73
16700	116.46		 	181.51	74.51
15955	105.87	86.17	73	183.02	
23523	254.3	77.51	75	184.72	39.26
15900	300.11	139.69	72	184.95	58.44
10545	272.15	72.91	74	188.26	35.42
16982	503.02	283.02	72	188.67	203.36
12848	147.36	47.97	70	188.99	42.1
5749	219.23	62.17	70	189.76	42.51
15004	289.65	146.93	71	189.87	51.07
23075	307.83	118.82	72	190.09	58.23
23584	123.89	91.92	73	190.24	73.31

TABLE 3A:	General Toxi	city		Document	Number 1650775
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
14997	311.34	155.46	77	193.29	31.96
7617	133.32	123.53	70	193.38	108.54
11404	425.93	237.07	74	193.8	75.57
14095	145.71	64.97	77	194.48	44.06
16766	128.68	62.34	72	197.3	64.57
13757	132.12	63.33	72	197.76	47.88
3981	165.72	126.27	71	199.27	79.29
6632	374.92	164.24	76	199.58	56.28
22770	344.97	196.08	74	199.66	52.17
1099	159.6	51.35	71	200.56	47.88
15170	132.07	62.08	79	201.16	44.18
21125	104.89	85.5	74	205.52	74.23
23499	149	73.65	71	206.76	68.16
16765	131.63	64.51	74	208.95	60.5
23321	173.83	57.63	71	209.49	31.61
18908	94.04	112.32	72	209.75	126.49
4360	159.27	76.32	72	212.18	102.53
5027	165.48	78.52	73	212.59	52.82
14007	147.14	73.93	77	213.84	62.97
4719	153.89	88.13	74	216.28	70.99
9754	78.35	97.33	75	218.88	111.68
5867	342.61	167.79	70	219.32	57.15
16859	374.28	189.12	73	220.43	60.14
24434	132.32	69.32	71	226.73	56.25
22683	206.07	65.39	71	228.15	41.78
13963	218.82	179.67	72	228.18	75.69
11179	165.79	72.22	70	230.16	61.5
23445	110.29	87.9	82	231.61	62.42
18115	174.03	108.43	71	231.75	102.05
11429	189.45	42.84	72	232.42	40.03
11520	175.16	127.89	72	233.8	92.23
7927	202.04	106.05	70	234.79	57.37
22099	137.03	97.01	71	235.76	97.02
7888	376.09	171.23	72	236.43	56.75
17496	75.49	73.53	76	239.51	173.47
11742	161.82	79.25	71	239.68	82.64
6855	194.24	59.54	71	245.57	58.27
22928	87.17	110.53	70	245.88	162.18
7064	397.22	140.47	77	247.28	40.15
10879	202.31	103.86	70	248.56	66.82
20757	401.81	200.88	71	249.74	57.1
7113	200.31	111.11	74	250.23	78.75
11635	186.84	60.17	75	254.75	47.63
135	174.94	73.25	78	256.19	65.78

TABLE 3A:	General Toxi	city		Document	Number 1650775
29656347	Tox Mean	SASSAULES S. S. SERVAN F. LURSPAN F. A. A.	\$ 2000 C 10.10. CONSESSOR 1 1/ 2000 CONSESSOR 1000 CONSESSOR 1	Non Tox Mean	800.000 NR. O 400.00000 - 400.00
24235	390.14	159.67	70	259.52	50.47
1479	205.28	61.98	72	261.61	51.03
5923	172.52	80.09	78	262.06	70.65
15642	368.73	123.22	77	262.87	41.31
9336	140.36	75.51	72	264.38	147.6
23325	326.83	125.56	70	265.55	63.28
9063	214.94	71.54	74	266.92	47.88
23612	382.82	255.62	72	267.25	92.93
912	326.5	67.38	73	268	33.47
14506	208.78	65.03	70	272.49	69.62
5748	328.41	66.67	70	274.63	44.97
8477	399.36	174.12	71	275.64	90.8
11021	177.75	93.53	73	275.95	97.97
8630	206.38	87.63	72	276.18	71.7
12331	142.97	91.35	73	276.42	113.01
12694	196.38	106.12	70	280.6	91.59
23380	201.35	91.04	71	280.63	98.56
25747	406.23	174.62	79	281.96	48.12
3418	416.76	178.28	75	282.48	51.77
19298	475.37	243.42	71	283.29	78.74
23558	187.58	94.53	72	284.57	75.57
6366	365.38	251.12	70	289.81	76.83
14103	153.89	84.24	76	291.22	113.41
24219	410.88	138.62	75	297.66	69
1929	232.96	81.98	71	298.56	77.17
5863	225.48	130.42	75	299.73	84.35
3504	395.85	157.69	70	301.1	58.36
4868	220.65	100.78	75	301.7	70.8
1753	235.94	62.13	72	304.05	74.62
22679	185.35	110.73	72	304.26	119.66
23230	431.68	274.8	77	305.51	73.66
17401	211.41	101.33	70	308.15	101.7
4179	444.58	228.79	73	308.58	63.03
24645	228.44	65.97	73	308.66	90.32
19679	212.7	94.25	74	309.08	79.13
8387	209.62	77.78	74	309.81	64.43
17324	236.31	65.13	73	311.13	52.23
1501	434.85	171.45	79	314.29	63.39
22582	224.5	87.58	71	316.36	75.3
25702	423.41	113.7	72	320.39	51.32
9399	222.67	63.69	76	320.67	86.48
3131	228.57	86.2	72	321.25	92.07
812	231.65	67.37	76	321.96	51.58
15519	303.98	284.36	71	322.04	142.67

TABLE 3A:	General Toxi	city		Document	Number 1650775
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
1409	258.93	68.93	72	323.5	60.85
17049	207.81	93.01	77	324.1	63.71
7003	213.89	133.94	75	328.74	101.01
15612	208.41	106.4	71	329.06	202.57
851	259.03	53.32	76	331.68	47.82
4291	203.94	139.04	77	334.29	127.4
1478	262.27	68.1	74	334.41	51.89
7868	201.78	131.72	80	338.05	94.52
19469	284.04	59.16	72	342.98	50.36
15700	259.03	65.96	77	345.34	50.31
15197	263	83.78	70	348.89	85.31
2484	152.64	144.08	75	349.45	189.22
21396	274.52	76.97	73	354.24	57.86
15032	262.98	104.76	72	354.96	94.2
6825	321.55	146.79	71	355.67	98.41
14767	212.27	97.6	80	359.19	95.6
15136	482.9	133.86	71	361.06	68.44
2993	498.11	173.18	73	362.5	53.1
1175	211.25	155.83	72	367.03	107.25
16680	296.57	157.31	71	368.4	135.7
961	300.69	83.8	73	370.86	65.28
2696	463.19	111.26	71	371.94	59.78
17256	266.11	96.28	72	373.05	70.36
4937		112.68	74	375.59	89.26
18860	305.59 314.98	128.88	70	375.92	92.09
23884	312.54	72.12	70	379.68	59.35
	516.17	220.77	70	383.69	72.82
17850 17175	504.94	132.64	72	384.43	64.15
12946	275.06	103.13	74	384.61	80.84
23322	308.64	91.46	73	385.69	58.02
16327	318.14	112.83	72	386.27	63.57
6824	820.68	540.91	70	386.87	102.09
1900	230.35	153.17	72	387.22	135.44
14869	290.26	114.01	70	388.39	93.33
15239	472.89	104.14	70	393.48	56.96
20694	256	155.8	75	396.34	127.36
6321	661.68	352.96	71	397.84	101.24
21157	628.44	255.63	70	401.01	132.71
1529		75.8	73	401.61	56.86
	316.33	<u> </u>	76	401.67	162.84
5934 19507	166.87	133.41 154.66	72	402.92	64.14
18597	452.56	 	70	·	114.82
6801	284.93	123.62	71	403.58	92.47
8317	302.02	115.59		404.94	125.39
3959	651.41	284.48	73	1404.94	120.03

TABLE 3A:	General Toxi	city		Document	Number 1650775
3857865 5	The second secon			Non Tox Mean	
6017	218.37	162.51	71	408.35	157.64
7785	309.16	154.16	71	411.11	92.69
18453	272.77	135.91	72	412.12	103.91
11157	347.22	111.72	73	412.71	76.32
2799	186.49	165.24	73	413.66	193.94
18606	551.54	140.45	71	415.6	65.98
25480	298.56	93.25	80	417.76	62.1
6554	327.78	86.42	75	418.15	72.16
22395	337.48	106	70	424.15	101.1
18861	353.52	146.94	71	431.18	96.34
556	363.95	72.87	72	431.39	47.74
15016	614.84	191.45	72	431.42	106
20707	297.52	182.87	72	432.6	110.59
6615	313.91	151.88	70	435.29	105.91
25675	559.03	149.18	71	435.84	78.46
24458	391.59	66.22	70	440.47	58.22
2264	348.28	114.55	70	442.01	101.65
811	339.77	83.76	80	442.46	54.75
14962	595.24	186.44	71	443.26	86.3
9905	351.99	86.2	73	443.66	62.13
4670	1011.12	757.17	70	449.34	279.51
15135	572.07	128.52	72	452.98	71.41
1877	381.72	99.89	72	455.58	70.01
2905	368.76	236.61	74	455.99	171.06
10176	362.61	131.62	73	458.21	78.68
8880	270.36	150.83	71	461.94	178.82
21977	333.82	102.68	78	464.63	71.57
19103	373.87	152.27	72	466.17	87.18
2505	361.86	109.11	73	466.31	72.15
7582	256.38	164.17	72	466.34	223.76
18001	369.81	89.98	72	467.77	75.36
15755	405.73	112.28	71	473.79	67.48
24577	583.7	137.54	73	474.11	65.9
20299	326.39	113.27	76	477.33	90.93
7697	273.75	100.92	83	481.09	117.81
18867	425.79	164.92	71	486.56	85.09
16726	386.57	78.35	71	489.29	90.61
18522	338.66	110.39	78	493.05	127.44
794	364.93	131.6	73	493.86	73.31
21097	596.6	213.78	72	494.87	76.63
11166	392.77	163.68	74	496.16	102.35
3823	819.94	253.21	84	496.62	131.46
20701	546.93	267.9	71	497.17	122.04
13283	374.45	137.36	71	498.65	90.97

TABLE 3A:	General Toxi	city		Document	Number 1650775
V 1 37 40 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	The second secon	Contract the second		Non Tox Mean	
14312	379.02	130.24	70	498.8	162.03
1561	489.56	192.41	70	503.1	74.48
11693	280.1	210.45	74	504.39	202.02
19470	355.43	120.62	75	507.23	102.75
20705	406.75	228.32	72	520.73	125.68
6060	377.46	110.54	75	524.04	95.02
4143	411.36	153.04	70	526.83	142.72
573	397.93	141.77	74	527.31	101.53
2111	431.14	135.97	70	535.18	95.74
6132	389.97	132.3	70	536.05	116.38
1531	432.89	99.85	74	537.37	84.23
13684	732.21	234.57	71	538.64	123.03
4914	320.44	176.4	77	542.57	159.28
16172	384.09	149.87	71	543.43	107
18661	375.83	155.78	71	546.25	136.03
14035	354.4	185.79	72	546.44	215.25
18452	376.32	156.49	75	548.91	124.57
10109	683.1	154.88	71	554.69	60.26
15113	422.52	185.06	72	557.21	136.1
12087	426.39	140.52	70	558.91	91.57
11492	398.17	152.29	73	559.08	143.79
14083	400.42	184.48	74	569.39	131.38
23961	487.24	102.51	71	571.23	72.66
6761	734.58	239.42	73	572.66	144.55
16993	402.56	131.25	80	574.27	86.25
11536	347.49	123.19	77	575.39	198.99
12312	415.93	131.04	75	579.26	98.18
20810	686.37	181.4	70	589.89	79.84
24771	441.44	127.76	75	592.18	94.5
6007	477.65	139.01	76	592.68	113.45
3145	432.3	212.79	72	610.87	178.16
12064	392.31	195.73	78	611.49	148.58
15080	468.83	133	74	613.82	131.38
22338	858.3	334.36	70	633.42	176.07
23437	417.21	173.85	75	633.59	238.89
20397	775.65	145.47	74	638.29	86.47
22930	206.34	282.8	72	638.83	389.14
5943	365.28	277.04	78	658.15	266.99
13088	440.35	191.07	72	659.11	130.73
3969	461.16	167.2	73	671.43	138.26
2536	229.18	164.07	75	680.76	402.5
8946			74	698.4	191.02
1173	488.94	198.29	73	701.71	147.85
	454.86	255.52	71		206.38
6613	475.14	319.24	[1]	703.21	200.30

TABLE 3A;	General Tox	icity		Document	Number 1650775
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
17847	587.34	146.42	73	728.57	116.89
19069	401.65	251.38	70	736.55	312.13
3121	582.17	314.22	75	743.82	177.43
2762	549.37	222.1	73	744.04	144.72
9191	353.85	236.51	80	747.6	226.01
17339	394.82	309.4	71	757.04	450.78
3365	465.6	196.26	75	759.09	201.02
5622	781.85	245.85	70	761.19	118.25
19729	390.13	332.32	78	764.27	355.89
9012	363.63	210.98	77	764.48	253.76
4193	592.69	173.22	72	771.85	108.77
8549	428.57	212.41	77	776.74	195.59
16190	633.77	300.61	71	788.33	198.05
6143	563.65	311.9	76	807.95	145.12
11228	611.37	254.64	71	817.25	249.82
19830	639.79	218.85	75	827.94	161.07
11504	659.77	278.75	70	831.93	222.74
2569	457.34	317.75	82	855.43	152.77
12160	812.82	573.26	70	864.88	230.19
21341	583.63	407.72	73	869.75	255.69
24321	471.3	256.45	83	871.6	204.88
14584	778.69	204.76	72	899.51	154.36
4440	592.51	190.31	81	903.2	141.99
17340	1192.58	780.31	70	918.51	258.08
2196	676.58	230.37	76	961.23	265.77
16879	875.19	424.83	74	998.63	195.4
14118	716.41	266.36	72	1006.89	263.75
20503	598.26	362.91	74	1021.64	320.28
12306	1122.58	844.77	71	1023.1	338.53
2911	675.36	278.69	72	1039.76	290.7
18796	825.55	557.51	70	1043.22	369.63
19732	639.42	377.16	74	1044.68	344.85
11205	763.23	299.36	72	1062.45	233.92
13634	1541.83	591.67	70	1065.68	230.26
8692	729.45	328.96	71	1075.69	284.09
22559	707.2	351.3	74	1078.43	298.05
9475	633.07	305.29	76	1091.11	321.49
6033	695.09	293.08	78	1093.71	230.15
7893	681.36	341.8	72	1123.77	299.15
3822	1790.91	546.55	78	1156.91	279.92
18910	691.91	316.7	77	1158.26	375.48
16703	811.27	347.36	78	1176.58	244.51
10984	769.03	347.66	74	1177.95	295.11
24162	935.19	218.55	71	1183.5	254.36

TABLE 3A:	General Toxi	city		Document	Number 1650775
			LDA Score		V
14960	1815.81	619.16	72	1189.85	282.97
22368	809.54	304.72	78	1204.44	255.44
14512	758.14	344.89	75	1207.73	316.98
22929	345.04	524.79	76	1263.79	749.31
6633	1158.38	523.64	70	1282.41	230.42
5899	868.41	419.97	75	1320.55	275.91
17027	885.56	416.43	74	1334.54	460.45
633	1120.93	302.27	71	1460.55	215.38
15240	1096.17	411.07	71	1507.99	426.62
3916	981.26	439.68	78	1583.55	340.89
22554	987.76	444.02	77	1595.12	393.47
3995	1025.02	387.98	75	1611.33	356.12
16885	1112.24	354.14	71	1613.71	341.53
9889	981.18	477.47	73	1620.07	396.24
15029	925.54	487.41	79	1688.81	378.2
6015	1123.82	384.91	78	1698.32	346
4330	991.16	483.62	84	1718.02	326.97
18909	1097.68	570.79	73	1735.42	607.51
3934	1109.15	552.14	74	1739.43	460.08
19363	867.12	620.13	74	1779.39	738.12
18002	1288.49	485.23	71	1800.22	448.73
4933	1364.86	630.42	74	1830.55	501.46
6380	1372.29	707.55	71	1841.36	514.23
16883	1363.62	527.7	78	2010.57	420.12
6072	1574.16	580.37	71	2013.52	377.64
17812	1417.56	569.56	70	2054.51	507.28
16701	1417.08	583.17	75	2071.93	447.2
6016	1345.93	620.12	75	2194.85	585.99
23261	1440.1	757.17	76	2245.13	579.05
9016	1484.15	791.38	72	2570.48	765.58
17524	1867.91	789.56	72	2578.07	684.86
22558	2228.15	660.37	73	3099.17	679.05
20502	2254.47	1019.37	72	3293.47	799.82

TABLE 3B:	Hepatitis-induc	ing and NSAIDS		Docume	nt Number 1650775
2 (27) (7)	Group Mean	2.1.000.01	LDA Score	Non Group Mean	
1661	41.81	18.92	85%	1.48	29.99
16317	30.67	11.58	80%	8.6	15.46
11893	54.33	34.89	85%	10.78	84.99
1507	46.98	9	89%	15.22	15.58
22966	36.69	8.83	81%	19.74	17.28
19671	37.69	7.44	85%	22.27	14.65
20016	36	8.96	81%	22.47	17.54
18495	49.47	12.55	87%	26.89	16.39
671	1.28	14.77	83%	29.18	22.7
1221	443.26	150.05	94%	31.23	89.26
25938	56.45	7.66	83%	32.22	17.92
18389	86.77	18.28	87%	33.41	32.92
11974	-0.81	15.18	84%	37.19	30.74
15834	-27.94	45.21	80%	40.53	65.46
20161	128.51	48.18	89%	43.77	57.9
17809	73.73	16.32	83%	46.32	27.65
7056	3.07	13.95	81%	47.6	27.96
5384	140.18	41.23	89%	47.78	62.23
16809		30.87	89%	53.12	26.62
	124.52		90%	54.32	20.04
11423	97.3	21.17	 		29.27
22918	25.37	5.71	92%	57.72	
20354	223.3	84.74	94%	65.21	49.13
18529	131.4	33.67	86%	68.42	53.24
1514	90.15	14.51	83%	70.26	23.25
8079	-4.51	23.75	93%	71.3	43.24
23847	116.7	16.84	84%	72.04	35.87
9712	23.03	12.25	88%	77.04	28.42
3660	16.83	21.57	82%	79.66	62.38
11904	167.34	25.7	93%	81.27	36.83
19158	45.35	20.66	81%	83.61	36.03
3710	-36.33	22.78	94%	85.53	112.55
15207	201.4	59.51	87%	87.46	53.13
18272	60.07	14.42	82%	88.02	33.03
353	141.35	40.91	85%	91.87	108.42
19410	151.13	23.55	87%	95.16	23.41
22321	170.96	42.18	92%	100.6	89.13
17277	197.62	54.02	87%	107.61	40.04
8597	164.65	22.23	88%	114.16	40.18
22151	53.9	21.51	85%	114.65	59.1
8274	76.86	17.29	87%	123.17	47.02
6532	271.93	51.51	94%	134.9	41.19
21570	190.77	30.4	81%	139.02	39.64
2555	331.4	107.66	92%	140.78	56.13
25370	84.18	22.52	80%	142.29	76.05

TABLE 31	B: Hepatitis-indu	cing and NSAID	S	Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
14208	94.74	20.59	84%	147.42	57.13
4250	206.6	31.57	81%	151.25	44.71
1521	259.23	49.47	85%	156.72	61.63
19075	223.09	35.39	81%	163.86	101.01
23584	77.34	44.36	81%	169.97	88.21
23855	348.59	60.39	85%	174.64	78.04
9595	340.35	75.95	82%	175.69	67.44
13332	103.75	23.14	88%	187.8	61.54
10544	215.74	17.73	83%	188.96	55.01
20914	95.15	42	80%	195.52	132.48
1796	121.33	29.79	82%	209	97.51
21039	106.61	32.3	84%	211.38	102.32
18891	79.72	50.3	84%	246.65	190.37
5464	135.66	32.82	82%	247.44	149.05
15786	143.55	47.13	84%	247.54	88.85
22619	538.26	124.75	87%	252.1	119.33
2655	82.89	32.9	90%	258.6	179.08
12156	181.92	29.95	83%	278.7	159.97
17664	741.68	141.39	92%	307.07	186.68
3504	500.63	92.33	90%	315.63	104.18
21281	205.42	64.7	81%	330.89	91.63
23890	215.59	58.3	82%	335.94	112.79
21663	239	51.32	81%	340.75	88.67
1795	160.6	58.49	90%	341.81	148.58
6825	186.43	50.61	90%	343.11	120.89
1900	172.64	60.15	81%	346.3	165.46
18465	620.04	89.19	89%	351.76	235.3
19412	785.76	148.65	93%	362.14	121.09
4026	890.4	293.19	94%	365.48	125.1
9148	247.98	44.83	82%	370.2	91.6
12928	537.35	88.04	83%	411.28	98.02
2905	272.3	68.62	83%	428.13	203.06
21657	770.91	200.72	85%	465.93	129.71
15127	328.43	46.16	84%	473.84	141.3
20701	957.82	322.59	85%	491.66	156.52
23125	211.15	54.99	87%	522.67	517.03
15606	391.12	82.13	80%	555.3	143.44
13557	380.72	110.05	84%	601.18	180.33
3365	412.07	116.59	83%	652.4	245.48
18890	249.81	125.41	88%	681.61	362.92
21740	1634.89	574.14	94%	692.6	269.8
3121	283.35	133.91	89%	701.53	256.63
16458	914	77.34	87%	721.93	196.36
11720	1413.34	300.55	94%	727.31	251.26

TABLE 3B:	Hepatitis-indu	ing and NSAIDS	Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11504	489.83	118.52	82%	806.57	268.81
17768	607.41	128.96	82%	831.34	168.24
13093	311.95	133.36	85%	873.19	562.27
6236	496.56	151.3	84%	902.06	432.96
23449	168.69	130.37	84%	927.26	659.99
23989	1753.97	311.2	89%	1058.6	400.01
23448	180.53	167.78	84%	1073.75	757.46
24289	653.83	137.29	88%	1100.08	340.79
16885	781.13	224.04	92%	1490.2	403.55
3917	948.73	233.94	87%	1606.37	494.39
6072	1216.55	290.18	86%	1863.45	506.08
9016	1131.05	452.13	84%	2271.36	942.23
6189	1001.77	624.81	84%	2994.32	1665.75
16884	1730.22	430.96	83%	3305.32	4446.34

TABLE 3C:	Necrosis and F	atty Liver		Docume	ent Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
7271	47.32	123.63	82%	-98.96	40.35
1727	109.71	134.11	80%	-50.93	105.7
5780	186.95	173.5	86%	-46.09	31.81
13203	59.69	60.36	82%	-17.7	44.77
16513	26.79	31.17	82%	-17.26	20.41
14619	43.31	34.51	85%	2.15	12.76
4553	26.34	19.46	83%	3.22	9.94
13458	45.73	26.41	89%	5.65	18.85
1610	44.15	19.04	83%	12.68	16.79
14693	74.3	48.25	83%	13.17	17.15
23679	133.75	76.1	90%	13.54	19.85
20456	59.55	30.52	86%	15.2	27.25
5733	152.59	121.24	80%	16.96	49.09
23435	130.84	87.29	81%	21.19	45.23
15312	97.29	57.4	83%	23.69	24.18
23678	101.95	55.99	89%	23.69	13.19
15861	71.17	46.83	82%	24.47	42.1
9181	83.64	43.77	86%	24.64	15.48
1598	201.08	146.9	80%	25.42	45.83
19940	83.79	44.07	83%	25.73	17.82
9796	72.8	40.14	82%	25.76	21.99
16085	106.34	47.32	89%	28.48	22.62
13467	155.47	95.96	86%	30.98	34.92
16618	94.85	58.13	80%	33.73	25.67
24710	86.03	43.14	83%	33.9	21
23260	157.52	100.81	83%	37.65	37.29
22876	70.57	22.75	82%	37.66	16.34
9331	80.05	31.38	80%	38.03	18.65
12614	139.71	71.97	88%	39.91	23.39
3280	81.33	28.39	81%	40.1	20.81
13874	88.42	37.45	84%	40.85	22.09
15862	84.57	34.63	80%	42.44	41.06
5926	80.04	27.03	83%	42.65	20.36
20449	254.92	200.63	82%	44.06	38.62
15313	148.78	79.95	82%	44.12	32.74
2897	110.58	50.4	86%	47.14	25.32
10549	203.78	148.01	82%	49.51	39.18
7243	132.31	62.02	80%	50.65	27.72
14939	115.22	49.92	83%	53.09	45.97
14242	118.61	49.19	85%	53.41	25.56
7161	136.07	72.13	81%	53.54	28.94
20708	91.32	26.75	86%	53.6	18.5
3831	104.66	45.67	83%	54.97	24.3
21707	135.19	53.83	81%	55.69	51.38

TABLE 3C:	Necrosis and F	atty Liver		Docum	ent Number 1650775
	·				Non Group Stdev
19264	117.33	44.24	83%	59.31	20.88
19150	109.31	32.72	86%	60.72	15.98
17687	99.1	21.62	85%	61.04	15.35
14462	156.22	62.83	84%	62.47	36.02
7036	131.87	57.57	81%	62.54	25.28
11527	177.9	80.35	84%	62.69	44.14
20082	124.7	51.02	84%	63.08	42.14
17736	432.83	313.35	81%	65.71	142.15
1841	136.63	50.08	81%	67.1	44.8
20523	102.48	38.3	83%	67.66	66.06
12965	169.8	78.23	83%	71.26	51.46
6085	208.53	104.4	83%	72.61	45.7
14458	330.83	217.41	83%	73.29	65.46
24236	184.01	75.75	85%	73.32	33.88
23160	176.55	75.81	83%	73.36	35.73
13251	323.03	180.5	84%	75.07	50.76
9784	153.22	64.68	82%	79.16	35.89
15398	239.17	147.09	84%	79.65	55.81
353	280.56	162.02	81%	80.59	90.86
20684	131.06	32.29	86%	86.62	20.64
14258	198.53	76.19	81%	87.06	38.11
22877	194.7	70.48	86%	93.61	36.71
1411	202.73	82.72	81%	98.83	39.17
11660	170.21	44.78	84%	99.62	34.3
23099	201.64	75.74	81%	104.62	41.86
23438	195.84	62.14	85%	104.93	43.18
17734	614.42	397.11	81%	110.47	174.81
7063	256.37	132.72	84%	114.31	69.93
1399	215.1	91.12	82%	116.84	76.67
5008	201.49	60.1	84%	118.38	36.13
11331	223.98	89.07	83%	120.5	40.92
25257	274.45	132.38	80%	121.28	48.13
16321	210.67	63.57	83%	124.13	43.97
20891	244.46	85.07	84%	125.01	52.71
2938	92.66	29.87	81%	127.24	29.13
22038	251.93	88.6	85%	127.34	44.31
17369	207.5	75.1	82%	129.13	60.27
5794	226.31	75.22	81%	130.44	40.81
5489	273.17	111.54	82%	136.39	59.55
20843	213.04	53.39	82%	136.57	33.06
2555	219.93	71.85	81%	139.38	59
15374	243.38	59.14	83%	141.32	44.16
24388	624.21	327.48	89%	143.82	68.72
22432	292.49	109.98	83%	146.05	50.66

TABLE 3C:	Necrosis and F	atty Liver		Docume	ent Number 1650775
	Group Mean			Non Group Mean	
18418	239.91	82.99	83%	146.58	40.53
12999	347.57	138.68	83%	153.73	65.66
26369	308.75	109.91	81%	154.12	55.73
14051	299.77	104	82%	156.87	52.25
4592	257.24	62.73	86%	157.37	38.03
4952	684.4	441.82	80%	158.99	145.89
23184	332.9	137.24	81%	159.3	52.72
7887	338.64	115.83	86%	162.05	60.73
18755	279.19	80.05	83%	163.56	53.86
17735	512.06	294.56	82%	167.32	151.69
4781	344.83	111.41	85%	169.37	65.78
22197	414.63	204.11	83%	169.48	88.02
23855	282.27	93.29	80%	171.07	75.56
14224	333.11	104.73	83%	174.8	67.56
6796	410.28	172.66	86%	185.7	72.52
20735	408.72	201.02	82%	185.89	74.3
21696	297.51	89.84	81%	186.09	42.02
11561	362.43	142.46	82%	188.78	64.86
3203	308.57	101.34	81%	194.76	46.19
7414	535.61	335.02	83%	197.35	92.11
15900	420.93	177.15	81%	202.45	80.18
23299	835.51	456.01	87%	214.06	131.12
2615	386.6	100.97	86%	217.6	65.98
5867	511.55	202.2	82%	233.57	78.63
24597	382.02	100.07	86%	233.91	54.34
11404	578.06	245.72	83%	238.77	146.51
1460	401.14	112.53	84%	244.96	91.82
498	416.48	120.92	83%	249.32	96.83
16859	472.45	162.72	81%	251.02	122.56
7888	537.76	182.29	85%	257.15	89.71
16756	553.61	229.09	83%	281.56	137.56
7064	502.34	176.81	85%	282.57	116.55
3418	612.35	201.12	86%	297.77	79.32
21458	1369.61	969.19	80%	306.95	224.17
2818	499.79	119.08	85%	321.5	81.64
23120	466.17	110.7	82%	322.94	76.21
4179	559.24	157.01	86%	323.2	127.86
21672	477.65	79.51	85%	327.31	77.78
23229	626.51	235.94	81%	338.12	95.94
1501	526.15	137.21	81%	342.01	115.25
7785	234.09	120.53	83%	402.39	211.3
6824	1330.86	651	84%	457.47	265.81
14962	735.07	188.78	85%	460.88	120.76
13646	647.84	120.93	81%	469.35	113.75

TABLE 3C:	Necrosis and I	atty Liver	Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11693	194.51	110.15	81%	475.41	349.8
6132	303.54	124.75	81%	496.77	136.48
7935	319.95	130.18	81%	539.48	150.81
4193	471.49	196.67	86%	732.69	138.33
2569	363.05	288.34	84%	741.53	276.55
6143	440.17	239.99	82%	761.21	219.76
20503	406.67	194.67	86%	913.12	368.79
16703	657.32	260.25	82%	1074.26	319.63
7403	747.37	603.65	82%	1275.15	420.96
7199	888.57	501.29	81%	1460.27	432.28
15029	731.54	467.45	85%	1526.56	513.26
4330	744.46	374.66	83%	1547.62	486.62
6380	907.19	397.41	84%	1723.63	601.93
16883	1078.56	580.73	82%	1877.14	516.54
6016	1048.32	457.34	84%	2002.18	710.82
23261	1133.22	790.5	81%	2083.71	702.84
9016	1179.45	473.8	81%	2319.89	929.08

TABLE 3D:	Necrosis With	or Without Fatty	Liver	Docume	ent Number 1650775
					Non Group Stdev
5780	149.44	174.82	83%	-46.61	31.66
14619	39.67	32.26	81%	1.81	12.49
5504	40.54	56.94	82%	4.45	12.06
13458	39.01	28.21	82%	5.58	18.92
15860	31.78	22.42	81%	6.3	24.49
14693	68.27	45.68	82%	12.72	16.78
23679	113.2	81.03	82%	13.37	19.88
15312	89.9	55.01	81%	23.16	23.77
15861	75.5	43.95	86%	23.4	41.45
9181	78.27	41.53	85%	24.18	14.99
16085	90.49	54.22	81%	28.58	22.73
13723	125.68	115.97	84%	29.26	45.67
23260	150.76	92.71	85%	36.36	35.87
9331	78.82	28.75	82%	37.48	18.21
12614	122.76	74.47	81%	39.76	23.36
13874	91.42	39.76	85%	39.87	20
15862	87.12	32.75	83%	41.59	40.71
2838	145.55	92.3	83%	42.77	33.6
15313	138.73	76.22	81%	43.33	32.1
2897	102.26	48.95	80%	46.84	25.34
10549	187.81	138.33	82%	48.44	38.17
14939	109.91	48.48	81%	52.56	45.94
14242	115.77	46.52	85%	52.64	24.7
17736	447.8	300.15	85%	58.86	128.94
19264	110.15	43.15	81%	59.01	20.79
14462	146.65	60.75	83%	61.81	35.78
15663	150.74	81.27	81%	61.88	28.94
13251	296.06	174.05	83%	73.46	48.79
6012	176.64	72.48	83%	84.55	40.71
22877	181.18	70.29	80%	93.15	36.67
1411	191.96	79.06	80%	98.12	38.82
11660	165	42.53	82%	98.96	34.06
17734	628.16	382.62	85%	101.62	156.16
6820	162.7	43.24	81%	105.26	24.87
1399	254.19	123.38	83%	112.16	66.1
7063	246.94	123.92	84%	112.9	69.1
24375	284.9	130.19	82%	122.22	50.94
22038	242.92	82.73	85%	126.16	43.47
15282	345.28	174.2	83%	133.39	77.83
20843	205.85	51.68	80%	135.98	32.8
11235	307.17	131.67	83%	138.32	42.12
15374	245.25	54.33	85%	139.6	42.14
8886	258.45	90.02	82%	140.07	40.87
24388	550.6	333.76	85%	142.43	67.72

TABLE 3D	Necrosis With	or Without Fatty	Liver	Docum	ent Number 1650775
GLGC ID				Non Group Mean	
6039	298.35	118.74	82%	149.78	54.28
26369	303.77	102.86	83%	152.16	53.29
14051	288.38	98.7	81%	155.61	51.3
4592	241.58	65.95	80%	157.11	38.16
17735	549.36	298.48	85%	159	133.2
7887	321.75	114.32	83%	160.72	59.56
18755	284.26	77.14	85%	161.37	50.75
4781	337.58	103.44	85%	167.27	63.76
20735	413.37	184.38	86%	182.1	67.45
7414	505.45	309.7	84%	194.61	89.53
11403	734.85	335.38	87%	196.39	177.82
15900	425.49	161.92	84%	198.73	74.48
15543	413.52	162.64	83%	212.02	73.08
23445	63.7	78.02	82%	213.22	89.74
6911	135.77	67.21	81%	214.68	51.49
11404	616.53	242.57	86%	230.44	130.03
5867	485.57	189.97	84%	231.42	77.22
1460	416.34	113.77	87%	241.33	86.89
7888	525.74	174.65	87%	253.82	84.82
26123	592.58	263.62	81%	267.76	130.29
16756	536.74	209.62	86%	278.76	136.63
24235	489.44	179.4	82%	280.21	94.54
3418	575.64	197.63	85%	295.93	78.26
19298	630.43	229.07	82%	317.49	143.34
23120	479.07	107.1	84%	319.7	71.63
2818	482.71	116.97	82%	320.15	81.06
15700	230.09	67.32	81%	324.4	64.93
228	236.54	61.87	80%	334.29	69.66
15032	205.99	56.82	80%	339.35	104.9
13294	644.35	170.98	82%	387.09	129.3
20707	228.73	113.6	81%	399.4	144.8
20299	283.13	98.83	81%	438.73	122.19
6824	1346.97	605.91	87%	442.76	235.61
14962	719.5	177.74	85%	457.94	118.72
794	301.18	105.82	81%	460.38	105.58
13646	650.4	113.01	84%	466.4	111.75
15135	628.19	146.12	81%	475.33	93.64
11693	181.61	105.42	82%	480.77	349.7
23390	900.94	286.52	82%	482.87	204.25
6132	287.11	119.69	84%	501.07	132.83
20705	268.91	129.82	81%	501.83	170.59
16518	745.69	208.61	80%	522.4	147.11
24501	924.14	324.29	81%	549.2	118.31
13684	940.24	251.12	84%	561.02	160.11

TABLE 3D	: Necrosis With	or Without Fatt	y Liver	Docum	ent Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
23961	413.97	100.86	81%	563.48	84.42
2350	914.43	280.02	83%	566.27	157.14
7262	1171.93	460.29	82%	616.91	222.19
15283	1210.53	436.26	84%	630.12	224.34
4193	484.87	182.86	85%	735.61	136.93
15365	1249.48	437.43	82'%	780.82	1098.83
24321	376.06	230.84	83%	789.46	268.88
22559	540.14	342.39	81%	1011.15	343.11
5899	694.24	374.16	80%	1263.41	404.09
7403	704.59	553.96	83%	1286.73	413.15
7199	835.65	469.87	84%	1473.34	421.86
15029	702.04	429.52	87%	1541.16	503.02
4330	675.9	370.63	85%	1565.51	467.91
18002	948.21	459.72	81%	1684.6	511.86
6380	882.65	369.95	86%	1738.14	594.45
16883	1007.86	547.7	85%	1895.14	498.99
6016	963.32	454.45	86%	2023.72	694.11
23261	1077.62	726.72	85%	2102.8	690.37
9016	1096.76	480.03	84%	2344.1	914.36
3062	1684.88	888.35	81%	2819.77	870.18

TARLE SEVI	Protein Adduct I	ormers		Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score		Non Group Stdev
26190	48.28	140.35	73%	-116.76	71.12
8700	49.85	77.95	72%	-12.19	36.84
1661	36.36	40.61	72%	1.43	29.6
18323	56.4	33.89	74%	6.38	36.18
4348	50.39	34.87	73%	11.17	31.72
	36.46	27.96	72%	13.35	33.51
17481		14.26	76%	13.66	16.78
5434	29.26		70%	17.21	18.45
5930	23.92	9.03			13.8
15778	24.37	10.62	70%	18.73	13.7
16251	28.52	7.89	78%	20.02	
23315	33.84	16.8	71%	20.08	11.03
23843	65.54	53.1	73%	20.76	16.77
24268	31.94	6.01	72%	20.84	19.94
12185	40.45	26.74	73%	21.92	18.47
6026	60.83	27.25	80%	21.94	33.9
9603	38.75	22.25	71%	21.97	31.16
17747	8.38	6.53	74%	22.43	16.15
21799	-5.84	13.09	81%	23.01	22.31
14195	36.74	19.21	73%	23.09	19.24
3976	17.49	10.74	71%	23.34	30.4
6533	32.77	10.84	73%	23.83	29.19
9166	69.93	53.74	72%	26.99	17.75
4610	63.26	38.33	71%	31.07	36.11
16167	26.11	7.76	73%	34.04	13.5
13967	69.09	21.43	77%	35.02	22.23
17677	-27.82	68.69	74%	36.4	69.93
14449	56.08	25.32	70%	37.77	22.83
11700	55.37	19.55	71%	38.12	21.59
1538	7.74	23.48	75%	38.59	30.39
14053	24.71	9.07	76%	39.07	22.35
6804	17.85	7.18	72%	40.39	128.09
15834	-16.44	51.96	73%	40.56	65.53
23170	43.49	9.26	75%	40.79	23.99
21823	40.81	9.62	70%	41.44	26.15
11485	76.43	21.72	79%	41.78	31.48
26288	55.27	10.43	70%	42.31	15.42
25409	8.36	31.39	76%	43.05	24.65
15251	38.39	9.43	76%	46.23	24.25
8124	57.68	9.64	72%	46.93	19.16
14126	34.95	11.94	71%	47.89	50.38
25203	29.38	13.58	73%	47.94	21.85
9432	100.75	48.6	73%	48.25	28.18
2153	74.75	38.6	74%	49.01	17.57
11127	51.39	6.96	73%	50.24	17.35

TABLE 3E: F	Protein Adduct F	ormers		Documer	nt Number 1650775
				Non Group Mean	Non Group Stdev
2933	50.64	8.95	72%	51.06	22.58
25615	71.69	18.81	70%	52.1	17.72
24654	81.41	24.85	75%	52.19	24.88
15018	84.77	83.88	71%	52.26	40.53
21707	126.24	73.39	70%	59.01	53.51
13918	98.73	44.7	74%	59.06	31.3
10549	42.34	9.93	70%	59.31	64.81
22566	92.71	49.39	70%	60.91	42.33
23304	84.45	28.37	70%	61.03	41.36
25413	37.94	16.74	79%	61.59	20.66
25410	30.99	21.26	78%	62.85	30.41
25411	27.66	23.64	80%	62.98	33.69
13581	83.19	33.57	71%	63.07	26.31
13932	-7.5	82.93	71%	63.9	55.62
14171	74.42	21.1	71%	64.55	37.62
90	36.07	18.79	70%	65.79	40.02
17257	114.03	67.46	70%	67.08	34.52
7537	58.32	14.12	77%	67.47	33.14
25397	33.74	21.21	73%	68.15	31.21
17894	82.35	13.84	78%	68.79	26.36
6814	89.6	32.08	73%	69.88	23.93
21893	44.34	8.05	72%	71.05	72.75
11438	111.77	49.88	74%	71.31	27.16
23324	87.26	41.21	73%	73.64	76.07
4168	104.37	21.68	75%	75.31	30.27
7903	30.15	21.43	74%	75.81	76.12
14335	83.34	14.3	71%	76.03	33.52
24589	112.98	48.88	76%	76.16	48.86
9712	59.65	43.73	73%	76.42	28.63
20980	95.23	16.77	71%	79.04	22.6
6003	97.63	17.55	73%	80.11	26.51
13175	132.4	51.99	72%	81.55	39.28
19315	140.15	42.44	84%	81.73	41.23
15156	110.09	19.69	72%	81.74	31.08
1169	63.7	12.97	72%	82.79	31.48
6032	51.63	16.54	72%	83.57	48.94
17400	145.45	66.75	71%	85.87	52.06
2006	25.42	45.67	71%	86.52	90.27
21068	264.69	160.27	72%	87.31	146.99
11215	-7.35	163.64	72%	87.87	83.21
3074	54.49	18.32	70%	88.91	83.5
22961	111.83	20.67	72%	89.09	31.98
2506	141.66	97.88	71%	91.9	70.92
6409	148.77	36.6	74%	92.24	57.46

TABLE 3E: I	Protein Adduct F	ormers		Documer	nt Number 1650775
GLGC ID					Non Group Stdev
22531	91.66	12.53	73%	93.27	36.37
21209	227.02	212.22	71%	95.2	92.15
2383	83.79	16.73	73%	102.14	37.31
11174	184.12	65.2	77%	102.16	98.46
17368	171.8	96.78	71%	103.87	47.72
20851	137.3	28.16	71%	104.02	55.43
3091	153.51	67.82	75%	104.92	90.83
18390	78.71	19.55	74%	106.46	50.88
3073	52.19	23.11	73%	106.62	118.05
6798	135.78	43.18	74%	106.64	46.11
14600	214.24	98.46	78%	109.92	74.91
17617	99.3	12.59	72%	110.02	31.44
14638	87.23	22.1	77%	111.45	74.07
10184	123.58	33.76	72%	112.37	55.43
9170	183.59	55.27	70%	114.2	52.72
22151	79.59	31.13	71%	114.31	59.46
	139.94	22.05	75%	114.56	32.47
12880		66.88	72%	114.75	41.55
14937	131.42		70%	115.31	58.59
2342	166.44	44.77			56.6
18612	131.39	23.5	75%	116.94	79.85
11691	62.73	41.24	71%	118	
17451	101.96	15.77	72%	120.36	30.67
19566	145.76	30.8	71%	120.45	44.75
24508	154.79	40.91	71%	123.72	32.09
1641	165.12	40.83	70%	128.2	35.55
23885	161.49	29.33	72%	129.48	47.42
20930	134.38	23.9	71%	130.09	61.62
5795	132.03	27.82	71%	130.17	53.46
22051	101.35	28.02	72%	130.68	67.38
26368	145.81	51.6	71%	132.19	91.73
19605	113.2	19.79	72%	133.82	51.82
21040	-18.07	52.54	71%	133.85	229.8
14776	102.58	34.94	70%	134.24	48.08
1223	182.79	51.88	71%	136.08	48.54
13762	158.63	98.43	77%	138.6	59.12
11048	119.54	22.24	73%	142.6	56.03
2292	84.06	42.12	70%	143.71	71.66
17844	277.9	176.64	73%	144.36	79.81
12215	204	107.83	71%	146.76	116.15
2043	179.12	22.45	78%	147.6	36.11
4157	177.19	33.3	74%	147.73	62.63
20711	228.01	78.2	72%	150.83	116.07
26088	145.54	50.27	74%	156.38	187.59
17572	159.65	44.25	71%	158.21	87.38

TABLE SEAL	Protein Adduct F	ormers		Docume	nt Number 1650775
GLGC ID					Non Group Stdev
1690	229.65	95.98	71%	160.28	60.57
15141	173.57	16.39	73%	162.21	36.81
16700	83.29	55.96	71%	162.48	108.7
20380	146.38	29.01	71%	163.02	57.5
15959	167.27	18.31	73%	166.48	70.66
9598	288.09	95.08	73%	168.1	93.9
11590	190.23	28.5	74%	168.24	68.73
22806	131.95	29.2	75%	169.43	77.82
18588	206.23	40.15	73%	170.98	65.63
1141	203.77	31.9	74%	172.68	35.21
9595	271.77	94.28	73%	176.57	69.08
24146	216.8	34.19	71%	177.31	65.74
17291	239.96	109.02	74%	177.33	137.8
21717	206.89	32.09	71%	189.62	69.87
13640	218.18	27.37	72%	190.6	71.83
	153.67	25.25	74%	191.38	72.77
14007		59.35	70%	194.57	50.93
16562	238.09	49.38	72%	198.22	88
10187	223.84		70%	214.98	65.34
25802	244.19	49.71	72%	216.12	86.16
11742	217.52	133.21		222.98	53.97
5020	191.66	26.95	72%	229.9	65.5
22603	221.37	90.45	71%		67.51
1728	238.87	23.07	75%	230.92	85.78
13534	182.27	33.55	75%	232.74	69.67
2868	286.73	53.61	71%	234.2	152.48
14997	375.7	196	72%	235.84	143.66
5111	393.78	167.65	73%	236.27	
20063	181.07	59.31	70%	236.39	97.14
16780	267.07	94.4	75%	242.2	64.47
23337	207.26	31.63	70%	243.84	91.24
19052	433.77	178.35	77%	253.21	91.88
22619	416.09	190.68	70%	253.69	121.24
6821	297.59	92.7	71%	255.52	167.53
17794	256.5	47.37	72%	259.54	87.89
5110	444.91	212.14	72%	270.46	106.82
4929	215.55	43.79	71%	270.62	101.5
23698	318.89	170.39	75%	278.46	123.55
10594	382.41	57.15	78%	291.69	58.26
6366	466.38	163.71	75%	301.16	141.67
5091	204.8	54.15	76%	305.72	121.65
12317	489.39	140.01	77%	306.86	86.66
15122	284.14	30.38	70%	308.23	65.78
2763	390	85.38	73%	308.26	88.64
20715	439.32	105.47	74%	310.12	180.07

TARLE SEVI	Protein Adduct	ormers		Docume	nt Number 1650775
GLGC ID				Non Group Mean	
25644	345.9	39.5	71%	314.7	121.98
1175	204.91	111.96	71%	321.32	143.78
24161	356.93	42.23	71%	327.71	79.09
18647	397.22	64.9	73%	330.24	91.79
21281	233.54	99.86	71%	330.78	91.46
4179	625.2	324.6	71%	330.92	127.34
43	237.61	86.82	75%	341.37	75.07
19458	364	43.15	72%	346.08	133.08
23128	313.06	51.91	71%	349.02	136.57
22412	366.89	96.19	71%	351.91	164.5
3143	483.63	141.06	72%	352.34	102.15
6801	355	56.71	70%	360.03	142.03
6066	431.59	75.6	72%	368.47	141.78
		63.41	73%	374.58	82.96
21575	432.67	158.85	72%	379.92	111.94
8317	421.43		71%	394.01	171.93
4371	507.88	124.44	70%	394.37	101.64
11157	373.15	134.06	72%	403.62	139.39
24296	481.18	92.3	 	408.23	71.6
556	373.54	45.1	71%	411.9	164.09
13055	482.08	75.69	75%		110.06
8173	519.73	67.84	74%	419.47	
3219	317.14	59.47	73%	426.13	99.03
16278	309.41	102.23	78%	429.92	164.15
23608	566.48	164.2	70%	431.27	241.18
25777	330.46	55.36	76%	441.54	130.73
18522	334.4	99.2	70%	443.31	151.76
6188	512.63	55.77	74%	448.02	139.04
794	333.35	131.81	72%	451.08	111.83
11693	254.85	149.73	72%	463	348.51
14312	397.8	81.06	71%	466.35	160.88
5339	852.55	606.3	72%	468.96	257.55
13646	546.37	100.3	71%	478.7	121.95
22534	444.69	49.89	76%	478.75	159.7
15121	635.12	147.29	73%	513.19	224.34
5038	398.62	86.39	71%	513.52	201.59
7916	483.75	53.88	76%	515.32	200.18
4759	421.47	104.72	71%	536.6	127.07
2339	519.32	64.43	73%	536.85	137.81
16947	444.15	113.82	74%	564.09	119.37
24707	469.06	76.22	77%	596.18	184.62
13557	472.83	125.45	74%	600	181.83
11322	781.82	176.95	71%	605.26	189.58
16623	815.06	113.69	75%	643.07	187.67
20397	756.19	106.73	71%	670.62	123.59

TABLE 3E:	Protein Adduct	Formers		Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
3121	513.81	224.23	72%	698	260.45
6673	697.31	124.67	71%	713.3	302.28
4193	655.24	191.97	71%	718.19	154.45
7552	709.86	131.78	73%	813.29	320.57
820	636.5	127.73	71%	821.94	204.55
19105	924.47	159.69	70%	829.48	236.56
16169	456.68	219.61	72%	862.69	796.4
20503	559	204.67	80%	889.74	380.31
6236	529.47	148.78	79%	903.06	433.66
16879	841.82	418.27	71%	946.87	285.04
17340	1644.38	815.75	74%	997.68	474.22
7451	1340.55	383.41	73%	1014.34	341.2
12306	1456.43	258.06	79%	1024.68	517.58
18905	880.62	169.73	78%	1175.6	278.99
17027	844.61	248.1	71%	1257.61	538.33
22554	997.94	184.01	86%	1359.91	523.26
26147	1510.64	528.64	72%	1410.78	338.29
9192	941.24	221.51	74%	1413.17	565.76
23243	872.48	380.03	72%	1417.04	675.7
16885	1012.98	320.39	72%	1487.91	407.92
15029	1042.74	622.16	70%	1488.18	539.06
4330	1083.48	398.15	72%	1508.27	516.11
22266	1415.56	499.05	71%	1514.02	441.93
18002	1259.73	300.25	77%	1637.82	545.26
4933	1137.93	526.28	71%	1700.05	608.74
21091	1307.31	329.46	70%	1706.98	564.25
6072	1518.7	338.39	72%	1859.25	511.2
17812	1406.92	373.38	70%	1884.53	608.25
17107	1929.94	1307.4	71%	2218.38	823.7
9016	1497.78	482.54	71%	2267.81	949.1
20846	2090.67	1066.14	76%	2478.45	898.34
22558	2580.09	1019.35	72%	2867.4	846.53
6189	1470.69	763.08	73%	2992.11	1673.91
11623	2359.03	1401.37	73%	3039.92	2772.61
16884	1876.68	541.26	76%	3308.78	4455.6
6018	1795.01	783.44	73%	3626.1	3303

TABLE 3F: A	NIT			Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22513	633.15	232.37	98%	-132.38	329.17
19388	29.83	17.06	91%	-25.03	31.57
72	49.9	30.74	90%	-17.96	34.45
489	86.15	31.02	99%	-11.18	21.72
11645	46.52	22.15	95%	-10.46	29.11
15003	103.65	34.94	91%	5.13	35.34
4318	23.26	6.71	91%	7.08	9.22
372	43.1	11.62	90%	10.4	12.2
14400	115.49	28.78	96%	12.11	47.49
15480	45.43	16.54	92%	12.38	8.62
22397	98.15	29.08	90%	18.38	61.47
23679	58.03	21.94	92%	20.39	39.25
10790	-79.79	34.37	91%	24	51.35
16006	71.89	13.1	93%	26.66	31.65
15701	115.07	45.82	92%	29.52	22.06
25052	170.78	53.79	98%	31.24	82.74
1221	221.03	65.82	92%	36.47	104.6
23945	98.4	22.42	91%	37.09	29.06
11608	68.37	11.81	92%	39.75	16.9
20741	140.96	42.97	91%	47.33	36.73
5384	110.15	33.33	91%	48.7	63.05
1809	660.39	204.87	91%	51.86	210.98
21088	88.49	15.38	90%	52.62	15.58
488	302.77	84.83	99%	55.29	40.85
20708	69.43	8.17	90%	55.72	21.17
11940	79.89	7.9	90%	56.21	16.71
6585	124.92	40.67	93%	56.76	84.64
15914	167.68	28.59	98%	58.06	29.32
1279	124.99	36.23	92%	60.16	22.09
22487	203.14	70.64	92%	66.54	38.82
17894	123.11	19.61	91%	68.4	25.56
2801	158.72	27.08	95%	68.44	49.17
14465	5.28	16.66	90%	70.62	29.14
15892	279.1	77.25	95%	73.2	79.81
7903	9.08	6.85	90%	75.62	75.73
20772	127.51	24.47	94%	79.34	26.84
11904	152.49	15.73	96%	81.95	37.81
23522	149.93	28.04	91%	84.93	35.96
14017	168.86	47.57	91%	94.1	25.48
23869	219.91	36.9	95%	98.3	110.47
14016	172.79	34.4	91%	101.88	27.02
23005	231.25	60.04	96%	102.75	100.99
24453	296.76	77.39	97%	107.86	52.64
23872	208.24	51.83	93%	110.93	125.84

TABLE 3F: A	NIT	The second		Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
10016	224.63	64.84	91%	116.67	48.65
17590	228.93	49.97	90%	127.17	38.31
4944	218.13	56.11	93%	129.57	134.8
15002	208.14	35.44	90%	134.25	36.07
20529	372.92	69.59	93%	138.52	121.65
20849	259.34	55.56	91%	150.94	38.19
15141	216.05	18.73	91%	161.78	36.17
15089	428.71	94.42	90%	164.31	111.52
24779	-119.55	53.79	90%	169.39	275.44
7665	325.89	51.47	94%	171.6	94
12577	530.07	99.18	92%	176.81	126.07
3253	242.21	21.26	92%	177.78	42.54
25069	384.72	63.15	96%	181.27	147.24
23182	70.96	27.02	90%	182.67	82.66
19043	461.37	93.08	91%	184.16	86.52
23445	44.92	13.64	96%	204.01	96.17
22928	18.25	13.42	90%	205.31	168.08
15300	301.52	31.01	95%	208.5	106.84
19073	357.79	55.66	90%	215.38	51.37
24237	602.69	44.81	99%	219.11	138.4
1447	293.32	18.87	94%	221.41	41.58
16408	151.08	35.06	90%	254.15	84.03
23868	529.77	129.48	90%	266.34	657.93
24810	103	36.24	90%	273.16	90.15
5235	460.06	75.16	90%	286.43	79.01
2802	498.79	58.22	95%	287.5	90.87
25747	698.21	163.03	91%	318.26	115.19
2818	510.22	88.82	94%	330.07	92.39
5934	42.22	26	94%	342.34	187.09
1501	711.93	121.22	96%	348.6	117.83
15535	499.6	40.24	91%	391.06	75.12
5437	327.15	25.07	90%	409.5	102.21
12928	607.12	43.69	97%	411.1	97.29
4207	611.82	98.48	90%	440.38	323.23
20701	762.37	110.98	94%	496.87	170.59
1562	360.31	37.96	90%	504.85	111.39
6824	806.51	180.29	90%	506.91	368.25
20983	343.07	66.3	93%	516.16	120.95
13088	199.67	54	96%	593.92	183.67
6613	320.2	65.66	92%	626.43	272.37
25024	451.39	46.56	91%	661.12	185.97
8549	262.14	62.15	93%	665.65	258.33
4193	484.74	47.1	95%	719.76	154.17
2569	257.19	110.15	91%	724.41	288.37

TABLE 3F:	ANIT		Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
7892	1166.36	244.14	92%	809.73	244.53
18900	1202.22	137.08	92%	830.76	217.68
16879	540.35	100.54	93%	949.72	286.7
475	635.1	94.59	92%	976.05	230.62
5899	704.5	125.15	92%	1227.29	427.31
3916	883.71	181.1	91%	1427.83	464.67
10378	2563.09	466.04	90%	1469.47	449.7
19363	372.52	212.88	90%	1539.84	830.44
6072	1270.16	177.57	91%	1859.03	508.9
20502	1504.84	383.84	91%	3017.48	1038.48

TABLE 3G:	Late Acetamino	phen		Docume	nt Number 1650775
GLGC ID		Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18028	62.86	12.89	98%	11.46	17.68
6151	41.98	5.06	97%	11.63	19.32
1394	46.55	7.94	98%	13.22	8.97
15701	104.85	30.26	98%	29.54	22.64
21586	129.12	22.29	98%	37.42	35.11
18099	74.54	10.03	98%	37.77	12.82
18990	191.58	50.21	98%	37.78	56
5492	154.99	36.3	98%	42.55	45.33
16958	152.1	24.97	99%	48.17	21.95
25892	5.84	14.89	97%	52.01	13.92
4281	8.04	4.69	97%	52.71	20.31
20817	552.74	204.49	99%	56.23	83.19
494	-58.87	15.28	99%	57.66	57
17091	221.12	37.22	99%	64.55	35.7
5493	201.07	32.69	98%	68.52	42.64
4650	257.12	41.99	98%	74.24	55.94
20818	387.65	157.18	99%	81.37	42.47
8356	191.89	39.3	98%	81.94	31.64
17090	166.91	23.91	98%	82.55	25.23
6153	47.01	7.23	98%	89.68	30.74
1399	422.27	102.52	97%	118.53	72.23
18369	14.78	33.12	98%	154.92	43.99
8107	82.52	12.58	99%	157.67	30.22
21305	78.03	11.47	97%	162.22	42.69
16219	91.23	10.22	97%	162.24	35.05
20380	51.46	16.74	97%	164.24	55.84
14970	64.35	7.2	98%	165.35	37.88
11039	22.92	14.76	98%	165.75	75.12
1644	69.04	14.22	99%	166.93	43.07
25632	23.75	9.64	100%	170.77	437.48
25069	648.62	107.28	98%	177.18	137.77
12848	77.84	12.22	98%	178.82	51.97
15571	37.5	7.71	100%	182.36	613.17
5998	82.64	16	98%	198.22	47.74
1542	75.63	15.75	97%	201.9	67.93
11429	113.75	15.07	97%	220.8	45.17
11635	84.37	10.31	100%	235.11	58.7
24246	680.67	154.62	97%	235.68	110.38
17684	115.68	11.83	97%	243.52	58.44
1479	111.19	13.1	98%	246.79	62.43
16023	118.74	16.82	97%	262.5	67.56
20986	100.65	16.03	98%	269.03	97.64
23033	164.75	20.5	97%	269.22	53.32
24810	78	27.42	97%	273.76	89.28

TABLE 3G:	Late Acetamino	phen		Docume	nt Number 1650775
GLGC ID			LDA Score	Non Group Mean	Non Group Stdev
8592	97.92	12.74	99%	275.69	78.69
12156	66.84	25.24	99%	279.94	158.15
20555		32.18	97%	280.75	96.14
18837	70.96	24.35	98%	281.18	112.85
17758	47.9	17.49	98%	283.74	151.83
11152	89.81	23.98	98%	284.55	88.62
22582	97.84	15.79	98%	290.41	88.62
6155	86.76	17.03	100%	302.82	149.97
10093	894.21	296.81	97%	307.41	125.35
23854	518.98	43.24	97%	317.71	83.8
4314	161.66	22.27	99%	325.66	70.88
20864	896.29	162.64	98%	340.85	169.02
9072	134.11	29.83	97%	372.6	132.4
15462	187.89	20.53	99%	377.51	69.64
3023	74.88	27.06	99%	377.75	123.14
1529	196.76	20.46	97%	378.11	72.49
24670	211.91	19.4	98%	380.22	75.72
25480	139.68	36.79	97%	384.92	88.4
4224	217.33	27.1	98%	385.39	68.02
1653	161.77	30.91	99%	413.84	133.06
9905	215.17	33.74	97%	417.78	81.53
11153	184.99	26.78	98%	424.64	112.76
21977	167.03	43.78	97%	425.7	100.74
21950	225.05	28.55	97%	431.25	83.14
2505	181.37	17.8	99%	437.97	99.3
794	185.22	23.41	98%	452.2	109.84
5920	1687.13	555.96	99%	456.93	241.47
2667	266.65	38.11	98%	472.54	95.54
24722	177.21	38.39	99%	491.55	112.03
23390	1178.14	133.27	98%	504.75	225.74
1562	261.12	32.84	98%	506.49	108.81
15113	155.11	52.14	98%	515.14	163.96
4199	289.55	26.97	98%	519.47	108.02
8872	1732.12	253.22	99%	539.58	281.13
24771	204.77	35.86	99%	548.56	123.7
13088	127.47	50.84	97%	595.53	180.73
17541	1185.11	145.34	98%	686.63	152.47
24811	244.05	55.21	98%	713.37	236.19
24321	133.15	53.97	98%	767.37	279.51
7552	180.78	39.85	98%	820.01	310.92
19732	145.53	28.91	98%	918.79	410.43
11205	330.78	77.32	97%	976.22	280.85
15673	1721.01	183.17	98%	1022.66	229.71
14512	230.44	36.6	99%	1088.1	390.72

TABLE 3G: Late Acetaminophen Document Number 16							
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev		
11850	2429.93	244.48	98%	1189.68	370.45		
633	647.11	128.95	97%	1346.47	304.28		
14960	3443.82	469.79	99%	1352.48	446.55		
22554	383.07	75.73	98%	1365.63	511.2		
24049	4317.73	1756.71	97%	1441.54	440.22		
2587	661.56	121.75	98%	1598.85	493.87		
12314	743.43	156.24	98%	2014.22	647.46		
15315	4723.83	784.41	97%	2482.27	635.01		
17730	6017.72	1076.55	98%	2933.25	821.08		
6189	422.42	136.09	97%	2994.06	1657.8		
20873	5487.66	1292.77	97%	3014.46	6409.47		

TADLE OUT	Early Acetomino	mban		Docume	ent Number 1650775
	Group Mean		LDA Score	Non Group Mean	Non Group Stdev
GLGC ID	8.2	4.71	94%	28.82	12.57
21175	8.32	4.93	95%	34.66	16.43
7528	-15.7	9.27	92%	36.02	33.93
20282		11.53	95%	36.31	21.84
5966	-2.42	6.89	92%	38.79	17.51
22695	10.13	5.65	94%	39.68	19.47
15634	1.39	5.3	94%	47.93	19.37
1520	15.99		94%	48.44	13.24
16524	20.02	6.63	95%	48.47	17.05
18482	16.24	5.44	93%	49.02	23.16
2280	19.83	5.96		50.55	15.04
19787	15.18	6.28	94%		23.14
18584	6.53	10.13	95%	51.53	14.76
13926	21.46	6.96	92%	52.65	19.95
11423	15.02	8.15	94%	56.28	
11940	21.79	9.2	93%	57.53	15.9
23000	22.53	12.08	93%	57.77	15.01
3080	-6.92	14.95	93%	58.31	48.7
23710	158.41	53.72	92%	58.38	71.02
23047	15.29	11.17	95%	58.49	16.56
16566	17.77	6.03	98%	58.51	15.69
19650	-70.3	47.02	93%	61.72	44.09
15467	11.36	7.01	95%	62.46	46.17
16728	14.72	12.75	92%	64.03	32.75
13568	28.12	10.02	94%	67.08	17.03
13932	-112.44	63.3	94%	67.38	48.47
15139	21.25	9.99	96%	68.11	25.84
24079	25.3	8.6	95%	69.08	26.17
22487	6.73	8.7	98%	70.08	41.42
14139	19.82	7.55	95%	71.65	22.54
15181	26.59	10.69	94%	79.78	30.61
23077	38.94	17.17	92%	81.22	21.14
17158	17.52	10.77	94%	83.01	45.36
20971	43.32	10.04	92%	83.29	21.37
1169	27.52	12.64	92%	83.96	30.23
16871	19.55	12.49	93%	85.46	26.85
9164	27.2	10.23	95%	85.81	27.4
15980	26.43	18.24	93%	86.7	23.87
16361	43.56	12.22	92%	91.15	25.64
21321	27.09	14.56	93%	105.32	56.02
3486	34.72	10.49	97%	107.9	41.25
2727	45.87	10.75	92%	110.53	48.76
8597	69.34	16.36	93%	116.43	40.21
574	65.57	6.51	93%	117.45	179.89
8730	45.4	17.81	92%	119.22	42.05

TABLE 3H:	Early Acetomine	ophen		Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
13351	36.93	12.29	95%	122.54	50.81
6330	28.64	17.18	98%	123.06	58.01
18829	33.89	17.14	94%	128.07	58.85
16134	18.36	24.36	94%	128.31	40.65
20975	70.64	13.75	93%	135.77	31.44
64	64.42	13.23	93%	141.31	35.51
11426	36.73	16.99	94%	143.85	61.64
4127	42.82	25.2	92%	147.26	55.78
2043	94.32	14.17	93%	149.89	35.38
25814	49.58	15.47	93%	150.18	60.26
23044	256.5	54.33	94%	154.34	33.61
23491	80.29	14.78	92%	156.45	57.06
21909	77.01	15.95	92%	157.72	48.89
16364	54.12	18.74	92%	161.04	68.62
6861	53.34	24.76	95%	173.75	47.49
23709	365.56	102.97	92%	174.65	139.26
18981	80.53	12.18	98%	180	124.54
18136	92.28	22.73	96%	180.63	44.47
15170	63.67	31	93%	182.69	57.04
15491	50.3	18.75	94%	184.71	62.38
13640	81.51	25.5	94%	194.43	69.6
1542	110.94	15.7	93%	202.72	68.33
23711	965.1	437.75	93%	203.15	366.12
3549	100.08	20.01	93%	203.26	64.36
5749	105.17	17.76	96%	203.46	50.97
1921	469.15	75.54	94%	203.88	88.71
5953	1395.67	589.94	92%	204.16	203.2
11179	51.98	16.53	97%	213.56	68.01
17571	121.22	22.36	91%	215.28	47.28
1919	540.5	142.58	94%	224.99	91
16449	-17.52	49.15	92%	225.71	118.83
7927	58.81	47.71	94%	235.03	77.05
8735	104.51	40.55	92%	260.2	118.96
15070	64.72	20.64	92%	276.22	127.77
23606	645.68	142.54	92%	308.45	97.73
4291	55.74	33.3	95%	309.48	143.72
6366	132.6	38.47	93%	309.95	143.06
22862	102.99	68.89	92%	331.29	84.1
1920	699.35	125.66	94%	334.22	116.2
23230	101.11	53.57	94%	347.39	161.95
1802	68.01	68.24	93%	348.21	129.62
1501	135.65	55.72	93%	359.59	120.35
3143	180.22	37.55	93%	360.43	101.81
20799	195.78	28.73	95%	368.39	68.29

TABLE 3H:	Early Acetomi	nophen	Docum	ent Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21980	205.1	26.69	96%	380.01	105.72
4234	728.11	88.4	91%	441.47	146.01
16215	277.82	31.3	92%	468.47	103.74
25705	303.85	36.79	95%	471.16	88.31
164	290.9	32.23	97%	476.12	84.6
21097	844.93	124.78	93%	521.05	142.52
23139	297.32	105.82	94%	614.3	226.46
8549	197.64	79.57	92%	674.01	251.68
9190	372.68	47.07	94%	1016.16	415.34
6291	552.9	84.63	97%	1091	307.85

TARLE 31- 1	ate Carbon Tetra	achloride		Docume	nt Number 1650775
GLGC ID		Group Stdev	I DA Score	Non Group Mean	
17064	50.24	16.97	96%	-4.18	20
1625	114.41	34.24	99%	0.07	12.89
5885	38.36	18.29	97%	1.99	9.82
18046	46.73	12.92	99%	2.71	14.04
16649	220.02	92.9	99%	3.43	37.53
1554	47.01	20.46	98%	4.33	6.64
20950	54.4	13.02	98%	6.19	12
13458	58.51	18.25	97%	6.84	20.17
6879	53.86	20.46	98%	10.45	8.61
2065	77.67	43.56	98%	14.07	10.39
16654	153.26	64.25	99%	14.11	9.91
23651	330.28	228.17	97%	21.42	37.58
15312	116.71	36.41	96%	25.99	29.2
21818	119.6	30.36	97%	26.66	21.99
4048	1573.97	2042.27	100%	28.72	92.76
21695	174.77	50.28	99%	30.87	22.35
1126	93.96	18.28	98%	31.78	16.86
17157	116.08	34.36	98%	33.37	18.38
21586	155.13	41.01	98%	35.85	31.46
4097	202.62	143.18	96%	36.77	20.82
20589	204.58	80.85	99%	39.66	14.51
4856	195.72	58.45	98%	44.87	22.87
17500	1.65	7.49	96%	45.77	44.45
16730	154.98	38.01	97%	46.39	26.25
20449	440.43	164.04	98%	47.45	46.4
15655	237.45	149.71	98%	48.19	26.25
19040	396.02	114.12	99%	54.95	29.77
1037	191.13	61.49	99%	55.16	22.83
4178	263.2	73.51	99%	58.46	46.4
23302	134	32.72	97%	60.71	24.04
21060	195.49	44.63	99%	66.73	22.3
2781	300.75	90.51	100%	67.08	21.7
1571	306.34	84.06	98%	69.24	44.27
1258	201.18	53.89	99%	69.76	26.45
20755	315.54	99.4	98%	70.92	37.08
21416	180.67	33.54	98%	71.26	32.81
4327	209.63	44.69	97%	73.46	30.98
2853	243.76	74.49	99%	79.5	27.62
14458	462.45	169.29	97%	79.77	81.9
17956	135.44	24.53	96%	80.41	19.61
16650	335.98	95.22	99%	82.71	42.71
8152	184.75	44.1	98%	84.34	21.12
22321	565.88	166.7	98%	90.43	44.8
20801	244.26	53.66	97%	93.54	45.27

TABLE 3I: L	ate Carbon Tetra	achloride		Docume	nt Number 1650775
GLGC ID		Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
15203	217.53	41.56	99%	94.08	22.2
16683	214.61	51.64	98%	96.97	26.38
7690	485.59	136.48	97%	98.07	100.2
18705	230.49	55.83	99%	103.84	19.16
574	566.67	151.26	99%	104.84	163.13
20644	284.09	69.38	96%	104.86	53.3
12613	385.02	81.17	98%	105.74	49.08
23173	527.13	156.81	99%	112.95	62.38
10016	305.83	117.64	98%	113.41	37.12
25257	401.37	69.21	98%	123.93	52.05
19377	245.39	39.45	98%	124.66	31.89
25313	368.62	55.36	99%	125.11	47.2
23888	323.47	71.72	99%	127.05	34.78
	f	65.27	98%	127.56	39.49
17754	280.21		96%	128.54	57.37
20891	284.25	57.73 61.55	99%	128.91	25.25
19241	305.11	28.1	96%	130.99	61.88
17369	251.93			131.28	173.33
4049	1800.21	615.67	99%	134.21	26.79
4426	226.63	33.81	98%	· · · · · · · · · · · · · · · · · · ·	88.42
15282	495.77	127.65	97%	140.76	33.86
20849	288.07	45.99	98%	148.97	51.3
17225	314.55	56.91	96%	156.73	
24388	756.8	218.92	98%	158.69	122.1
16854	274.55	32.55	98%	161.83	29.13
16610	376.93	79.48	97%	165.18	49.27
6193	447.67	59.78	99%	194.57	54.15
3549	368.01	54.43	97%	196.19	60.45
2744	487.89	65.94	98%	202.98	55.42
15281	509.13	65.19	98%	207.9	69.15
17571	337.5	57.58	97%	209.52	44.91
8928	323.46	31.08	98%	210.05	36.77
25802	411.96	57.18	98%	210.79	57.41
12551	48.43	13.62	98%	212.69	71.68
7602	453.04	80.74	97%	213.06	62.29
15543	555.28	110.77	97%	219.06	83.33
958	492.73	90.77	98%	234.42	59.68
2854	520.08	129.87	99%	239.21	54.99
5331	517.46	66.57	99%	253.08	62.49
23013	631.62	255.14	98%	253.69	77.98
19768	497.6	88.61	97%	258.31	86.39
18107	475.79	86.06	98%	270.37	50.73
10306	537.72	79	97%	270.7	72.51
3138	773.53	129.57	99%	280.59	128.8
16684	591.01	105.06	98%	303.32	77.67

TABLE 31:	Late Carbon Te	rachloride	Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
23854	563.93	104.51	97%	314.55	77.09
20897	602.65	120.81	96%	315.7	85.83
19298	835.39	188.74	97%	328.8	152.97
25718	579.2	77.87	98%	328.95	68.42
14959	676.74	116.99	97%	377.46	94.35
20879	73.93	55.35	98%	390.34	126.05
6824	1794.5	585.37	97%	479.02	298.25
13684	1052.78	207.71	96%	578.09	181.33
16438	1299.24	155.02	99%	582.93	144.92
4193	332.28	95.67	96%	726.26	144.3
7552	163.75	89.31	97%	826.93	304.52
16883	681.46	275.09	96%	1856.78	528.87

TARLE 3.1	Early Carbon Te	trachloride		Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev			Non Group Stdev
8663	721.93	225.97	97%	-87.65	146.96
8662	653.64	143.71	99%	-66.58	95.42
1727	348.89	185.42	95%	-57.26	75.16
11493	129.55	67.26	96%	-32.97	39.87
2628	251.75	147.92	96%	8.65	34
15647	109.5	26.81	94%	11.25	155.64
13265	78.29	37.64	97%	12.05	9.28
923	199.22	94.23	95%	15.81	23.49
8661	614.42	215.98	99%	16.84	60.47
7301	187.05	149.7	95%	19.02	15.94
15312	129.52	34.52	94%	23.98	24.69
	159.8	80	94%	27.12	24.91
1305 1598	232.56	58.02	96%	28.01	58.64
		595.26	94%	30.79	97.73
23567	918.41		97%	31.18	21.37
25198	145.62	46.46	96%	32.31	38.97
22443	413.57	187.24		33	26.32
809	170.72	83.79	94%	 	27.16
18043	157.01	66.2	95%	35.05	15.49
16825	86.21	14.87	95%	36.95	
11494	365.78	87.61	98%	39.57	52.58
12969	315.69	145.09	97%	39.62	30.17
347	94.32	20.45	94%	44.31	19.5
15313	188.23	47.79	95%	44.81	34.49
25907	196.63	51.46	96%	45.95	29.69
2629	258.22	130.51	94%	47.27	31.18
4119	172.99	53.46	96%	49.1	27.57
15617	131.28	26.96	94%	49.13	28.01
11483	356.15	129.53	95%	49.85	57.22
25098	263.21	101.83	95%	51.71	35.09
8664	685.72	187.22	98%	51.77	117.57
7806	173.92	56.36	95%	51.78	24.26
5932	142.26	26.26	94%	51.91	24.37
18501	128.83	31.95	94%	53.7	17.47
352	306.66	117.09	94%	53.93	48.46
3831	120.45	24.02	95%	55.42	25.76
651	234.03	95.8	96%	55.88	31.26
650	252.68	84.65	96%	57.08	37.09
17337	140.87	38.01	95%	60.97	56.3
7036	176.78	42.65	98%	62.22	22.87
22124	125.04	23.89	94%	64.53	17.38
23587	208.43	60.7	94%	66.37	32.19
21130	369.23	131.33	98%	72.63	40.41
353	475.4	152.81	94%	76.96	69.6
1183	426.68	140.86	99%	78.14	33.96

TARIF 31. I	arly Carbon Te	rachloride		Documer	nt Number 1650775
	Group Mean		LDA Score	Non Group Mean	Non Group Stdev
16080	464.2	128.58	94%		87.93
18349	210.66	61.07	98%	82.84	26.6
19184	623.72	284.24	97%	83.93	71.71
	214.08	67.37	95%	87.98	29.5
2788	225.71	67.73	96%	89.73	24.64
15291		36.2	95%	90.84	24.55
21380	195.27	67.94	99%	91.5	64.42
17908	489.98		94%	95.88	162.38
1475	764.62	270.51	94%	96.35	76.24
354	549.22	181.76			294.14
14424	1887.85	604.98	95%	104.46	42.63
23438	233.78	45.73	94%	105.37	34.08
19085	235.47	46.91	96%	105.97	
16318	569.79	137.14	98%	106.93	68.65
19641	354.6	119.72	94%	111.15	52.02
2049	351.74	96.17	96%	113.35	54.16
22625	588.59	137.7	98%	119.99	73.04
15616	363.79	100.12	94%	126.33	57.91
16081	590.52	148.03	94%	131.04	114.9
1306	354.57	112.94	96%	131.39	47.78
5489	361.63	79.95	96%	135.76	55.44
19086	312.97	47.23	96%	137.05	43.97
22681	1733.5	1045.76	94%	138.8	233.99
25567	440.46	120.5	94%	146.39	68.31
5820	392.73	112.42	94%	148.03	58.75
19075	541.95	182.12	95%	149.36	55.34
8314	4119.47	2769.99	98%	151.41	501.27
24234	520.49	130.96	97%	152.5	60.67
15490	337.2	71.58	94%	153.12	62.58
18259	558.61	152.63	96%	160.23	83.57
4952	867.67	202.68	94%	163.05	167.45
20795	498.26	84.68	97%	165.95	99.22
15292	331.21	64.99	94%	168.13	43.41
17735	616.97	206.23	95%	170.62	159.27
15382	2086.55	655.12	96%	179.06	342.56
6892	472.18	95.02	96%	185.03	58.03
10019	573.47	205.58	98%	186.54	69.46
8984	284.45	40.11	94%	186.61	41.02
3587	1589.64	832.55	95%	189.25	164.29
23331	343.71	75.44	96%	197.53	41.31
17753	422.58	107.22	94%	199.72	55.6
3430	482.45	99.02	96%	205.47	61.75
5937	398.98	79.16	95%	210.95	55.18
15091	457.85	75.14	94%	214.95	79.48
2615	475.24	65.04	95%	217.68	61.55

TABLE 3J:	Early Carbon T	etrachloride	Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22177	437.19	83.23	94%	220.99	76.02
15558	421.96	49.45	96%	261.21	89.18
15171	2476.94	637.89	99%	267.37	221.89
24235	651.38	135.2	94%	281.24	89.88
15172	1130.82	386.63	99%	294.17	160.06
8665	2451.27	808.98	94%	320.3	582.92
3816	941.08	189.07	97%	375.12	97.06
15051	1917.64	600.05	97%	421.84	274.9
6321	1227.19	294.21	96%	436.54	171.1
11495	1157.08	222.69	95%	479.89	170.9
19012	1131.9	195.46	95%	491.44	164.34
3139	3078.65	1586.03	96%	683.5	401.95

TARLE 3K.	Late Cyprotero	ne Acetate		Docume	nt Number 1650775
GLGC ID	Group Mean		LDA Score		Non Group Stdev
25183	57.99	11.18	99%	-65.21	41.14
9969	66.32	43.47	97%	-28.99	30.94
19292	39.25	15.99	99%	-0.31	8.76
1749	36.95	4.96	97%	6.56	12.85
9697	56.57	15.67	98%	10.84	13.14
19465	72.95	28.72	97%	20.05	13.1
15441	57.11	16.22	98%	20.18	10.67
15987	363.79	45.36	100%	34.51	32.07
13580	0.18	7.99	96%	36.01	21.03
16319	89.11	16.96	97%	40.72	16.75
3510	7.29	10.94	97%	41.17	13.42
906	86.53	14.25	98%	49.56	12.1
19053	13.57	5.47	95%	50.36	50.88
5824	209.96	52.5	99%	54.58	27.78
17685	17.67	8.55	98%	59.93	29.82
4588	22.45	6.38	97%	60.62	24.09
14250	25.11	4.35	96%	61.29	33.6
17091	228.81	44.44	99%	65.14	36.75
4312	458.51	102.72	98%	74.88	65.39
6667	35.58	7.42	95%	79.42	27.4
9668	25.68	7.88	95%	82.74	43.74
17090	174.43	31.41	98%	82.84	25.5
14840	25.84	4.54	97%	84.25	56.66
18906	165.1	25.73	97%	86.57	33.68
21184	24.35	7.77	96%	88.84	44.65
11960	-21.76	29.8	98%	91.47	36.61
17092	282.98	55.61	99%	100.94	37.11
18316	41.41	4.56	96%	101.42	51.02
11724	26.29	6.1	97%	107.83	53.24
21238	29.51	14.62	96%	107.94	65.27
9015	50.88	4.22	97%	111.21	39.72
22204	31.75	11.16	96%	111.85	67.38
21228	60.32	10.12	95%	127.7	59.24
25725	303.56	97.38	99%	127.99	39.22
3381	215.51	15.65	98%	129.07	31.01
14199	49.89	11.18	96%	129.55	63.16
12158	539.59	79.37	98%	149.3	94.76
20711	15.4	13.95	97%	153.96	115.63
25055	543.96	83.34	98%	160.37	97.11
15955	401.03	64.61	97%	167.69	104.75
10002	79.22	8.3	96%	169.5	85.35
15888	103.8	7.37	96%	174.62	107.57
23709	91.99	7.53	96%	180.95	142.33
19255	96.69	11.59	96%	191.17	81.51

TADI E SK.	Late Cyprotero	ne Acetate		Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
16124	59.91	18.31	97%	198.11	129.25
8053	55.5	21.16	95%	199.73	121.49
1796	713.84	124.8	99%	202.3	82.74
6431	44.99	10.12	99%	211.22	232.8
	60.8	23.4	95%	213.43	78.15
4576	83.58	18.05	96%	218.87	74.81
22713		37.25	100%	230.7	84.72
20803	489.88	13.33	96%	236.42	105.34
8905	129.45	115.87	98%	240.36	60.06
16780	482.97		96%	245.89	63.54
1479	143.4	14.02	98%	270.19	144.04
12156	947.53	169.32		271.87	106.81
24860	762.67	137.57	99%	277.11	153.4
20744	131.35	9.57	96%	295.84	176.52
12157	890.46	241.3	96%	·	93.48
19256	169.36	16.84	97%	300.56	112.43
12155	849.1	121.68	98%	328.83	138.76
1795	886.32	169.03	98%	332.97	
20864	838.11	192.14	98%	343.82	174.37
23032	174.66	35.02	96%	348.75	98.36
18860	658.47	93.14	97%	352.87	102.72
6801	167.82	26.32	95%	361.85	140
20915	707.08	113.27	95%	376.44	136.93
20707	836.46	117.26	98%	382.05	142.91
18473	830.53	86.28	99%	405.69	223.02
16278	872.29	116.7	98%	422.72	158.18
20041	189.58	32.85	98%	435.36	136.08
25056	1055.84	195.39	98%	435.67	129.34
20714	148.21	41.46	96%	438.15	637.41
15500	239.22	24.81	97%	456.63	119.52
15755	214.37	34.27	99%	457.32	99.49
11693	37.65	37.02	96%	462.5	345.74
15127	911.94	86.23	98%	466.74	134.84
21078	321.33	18.18	96%	470.87	98.57
19012	218.63	26.43	98%	519.87	206.37
20713	192.33	64.34	97%	523.9	200.74
8872	2206.69	222.08	99%	539.95	267.56
1551	300.22	24.52	98%	540.56	133.08
15391	748.88	48.29	98%	555.42	79.76
17541	1121.82	231.52	96%	689.41	156.88
2569	1283.55	169.03	96%	712.78	286.97
20804	2441.26	676.23	98%	723.52	393.32
12160	2592.66	403.1	99%	826.97	370.84
11644	421.94	97.8	96%	834	240.59
17788	2318.81	523.51	98%	909.78	263.72

TABLE 3K	: Late Cyproter	one Acetate	Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
17117	1568.35	191.58	96%	1006.34	230.44
15645	474.3	53.72	99%	1085.08	601.13
6479	446.51	75.83	98%	1215.32	472.08
22266	2441.41	319.93	97%	1502.46	434.41
21798	2671.47	378.77	98%	1532.27	351.77
1957	451.84	140.88	95%	1533.47	786.6

TARLE 31 :	Early Cyprotero	ne Acetate		Docume	nt Number 1650775
GLGC ID	Group Mean			Non Group Mean	Non Group Stdev
12375	39.55	6.91	93%	6.16	21.17
2803	101.95	30.32	98%	12.74	30.67
18685	55.02	18.44	95%	16.95	33.49
15162	38.84	5.14	93%	19.37	14.99
10200	71.52	14.25	98%	21.52	18.12
11619	40.76	5.29	93%	24.39	9.81
5018	43.56	9.08	93%	25.12	11.36
11125	95.81	17.05	97%	28.28	20.68
25706	108.93	17.96	98%	28.74	24.94
17506	202.1	34.4	99%	28.98	70.24
25852	57.42	8.81	96%	29.52	10.16
16783	107.34	24.04	95%	33.35	33.97
4725	93.9	10.69	96%	40.84	123.37
15097	97.88	13.08	95%	42.76	28.79
2594	115.78	19.67	97%	43.16	28.35
18484	139.66	35.48	98%	43.46	17.72
7967	80.61	8.41	93%	45.01	25.09
15251	113.13	7.4	98%	45.58	23.44
14913	104.39	13.3	94%	51.71	28.53
15655	103.19	9.18	98%	52.4	44.96
5740	98.42	10.02	93%	54.17	22.49
	88.27	7.53	96%	55.12	26.88
15433 6676	81.6	7.48	94%	55.36	26.6
12203	284.85	67.35	98%	57.37	50.59
11876	164.99	37.72	97%	59.91	38.15
24051	156.13	27.52	97%	60.29	28.94
24227	159.76	22.26	98%	64.47	29.99
23160	140.18	19.33	94%	79.22	46.25
24236	118.22	13	94%	79.8	46.11
5754	354.87	77.25	99%	82.05	52.7
5046	201.39	29.93	96%	91.8	52.22
4679	155.83	15.02	94%	93.09	39.05
2372	227.9	45.92	97%	99.62	37.53
466	147.74	16.09	93%	100.97	24.77
9128	497.34	121.83	99%	101.85	43.69
16087	72.43	6.68	96%	105.7	17.95
22898	203.84	9.33	98%	107.87	73.23
22717	160.84	13.59	94%	114.08	91.92
9775	472.31	82.29	98%	118.73	84.58
19605	335.27	35.78	99%	131.91	48.58
22503	297.45	72.36	96%	134.1	70.26
1903	323.28	80.7	97%	134.88	55.57
<u> </u>	298.97	43.04	96%	137.13	83.58
6582		7.66	94%	138.35	50.24
15030	<u> </u> 175.94	11.00	J4 /0	130.00	100.27

TARLE SI :	Early Cyprotero	ne Acetate		Docume	ent Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18235	287.07	66.63	97%	138.94	38.25
15282	203.3	21.11	94%	148.94	105
13799	391.75	74.97	99%	152.36	52.97
17955	257.17	57.57	93%	154.46	62.37
6272	415.31	82.23	98%	157.51	61.87
3266	238.25	22.7	93%	160.5	50.15
15959	389.2	63.99	97%	164.9	67.38
1884	191.9	7.86	93%	166.42	45.16
15955	294.4	26.85	95%	169.12	106.78
9486	468.68	91.29	94%	177.99	126.67
21275	349.64	80.81	96%	178.44	97.42
16053	311.13	32.05	96%	206.21	223.6
16747	445.78	87.8	96%	210.09	78.61
	393.34	72.05	94%	217.18	69.07
20350	290.54	8.31	95%	227.55	64.59
6855	437.32	39.57	98%	229.27	188.62
2326		78.7	98%	232.67	92.42
20063	579.31	85.89	93%	235.8	240.72
11403	386.09	38.02	94%	240.55	89.2
14303	381.51	17.35	93%	246.96	110.75
5696	167.33		95%	247.96	137.64
7586	568.83	104.54	96%	253.55	163
6821	667.02	106.37	96%	256.59	86.57
12956	525.48	76.44		257.84	173.77
11404	487.51	32.83	97%	269.02	120.09
4092	428.51	31.72	96%		77.1
20	182.6	13.17	93%	280.26	136.85
7003	480.07	48.06	93%	299.91	87.86
22835	515.95	104.87	95%	316.8	119.46
22235	511.17	15.69	98%	321.64	159.22
1900	909.26	49.41	99%	339.05	
9674	997.96	198.11	93%	345.29	332.5
2757	553.61	62.46	93%	349.8	112.21
3233	469.14	29.71	94%	350.16	111.19
4937	644.14	96.95	97%	351.09	99.81
16688	485.77	14.98	95%	367.52	115.86
8215	528.57	63.29	95%	395.11	169.02
23515	527.7	47.35	94%	399.57	182.28
22548	1110.25	157.18	97%	429.36	198.23
25056	701.5	107.45	94%	439.98	142.37
23030	298.12	25.05	94%	443.27	320.1
1930	795.75	79.48	96%	488.29	180.53
22379	987.52	105.4	98%	497.46	281.53
18280	625.22	42.6	95%	500.51	355.18
13557	431.55	35.49	94%	598.3	181.76

TABLE 3L:	Early Cyproter	one Acetate	Docum	ent Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1901	1382.54	291.7	97%	621.54	268.35
16205	433.92	33.39	96%	622.45	128.79
19069	172.52	18.28	97%	622.95	345.06
22906	1189.14	110.88	96%	633	508.28
7262	974.62	93.19	94%	656.38	287.35
2354	1225.56	104.8	96%	666.98	252.59
7362	563.59	37.8	94%	816.77	299.68
15345	1802.55	235.04	95%	907.53	318.35
3803	1252.52	61.21	95%	914.67	209.78
22929	620.51	53.83	95%	1008.19	813.54

TARLE SM: I	Late Diclofena			Docume	ent Number 1650775
		Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22513	2558.9	1121.55	99%	-137.91	262.53
19512	46.17	16.3	99%	-20.41	27.06
8700	150.91	57.74	98%	-11.7	37.23
19715	70.75	11.06	98%	-11.14	18.14
	79.3	16.37	99%	-10.24	29
11645	64.31	15.52	98%	-7.94	37.09
20200		32.07	99%	-1.01	21.41
7858	64.65		99%	0.06	50.52
22516	230.66	81.61		1.86	14
18974	52.85	14.89	98%	7.46	12.49
5291	56.16	15.92	98%		16.15
9977	33.87	1.2	99%	9.6	
372	53.19	3.15	99%	10.58	12.35
14400	168.71	36.04	98%	12.55	47.33
955	44.09	5.41	98%	13.21	12.09
26320	148.57	67.07	98%	20.83	30.04
23555	177.11	52.37	99%	22.61	21.13
10790	-147.58	11.69	99%	23.65	51
21445	152.54	38.45	99%	24.94	41.96
16173	102.32	21.29	99%	25.18	32.39
25052	653.33	363.97	98%	29.48	65.56
3452	158.59	24.76	99%	29.79	27.82
12277	126.55	32.95	98%	30.14	31.31
16240	-1.46	1.38	98%	31.65	28.31
22512	280.38	149.23	99%	44.34	59.45
7056	-11.07	4.54	99%	47.11	28.14
19411	117.91	13.87	98%	47.27	27.38
6198	184.84	21.67	99%	47.55	71.13
25246	17.4	2.21	98%	50.19	18.57
15504	223.77	86.68	98%	54.96	108.78
22514	404.55	221.07	99%	61.23	63.25
13045	-1.13	17.95	98%	64.8	29.82
9826	-2.67	5.61	99%	66.89	26.12
8079	-12.12	4.26	99%	70.37	43.83
2310	520.93	356.23	98%	71.67	85.7
25290	159.42	12.09	98%	74.09	78.6
1430	-67.02	9.22	98%	76.13	70.5
13895	199.32	16.84	98%	81.85	53.19
11904	162.22	8.31	98%	82.4	38.06
11596	208.15	21.91	98%	92.32	36.27
22515	1549.73	711.86	98%	100.85	133.92
22321	175.23	33.28	98%	101.48	89.03
8522	399.56	124.51	99%	108.85	69.48
14491	261.16	27.37	98%	115.78	52.28
21228	330.87	20.94	99%	125.87	57.45

TABLE 3M:	Late Diclofena	C		Docume	ent Number 1650775
GLGC ID		Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
20529	887	406.86	98%	137.26	107.43
3250	366.5	30.94	99%	144.45	58.3
14504	691.37	422.61	99%	151.43	95.9
26133	549.15	106.67	98%	153.02	280.02
21978	81	5.94	98%	160.08	42.54
3708	397.54	42.39	98%	161.72	77.01
396	355.91	58.85	98%	172.48	57.78
23889	72.55	12	99%	175.14	49.66
12577	1097.35	411.24	98%	176.09	109.22
18580	822.77	189.24	98%	201.23	172.81
24237	928.14	321.39	98%	219.99	132.72
25618	180.02	2.6	98%	245.62	81.24
4969	1833.13	949.96	98%	265.19	240.61
5110	738.94	147.68	98%	271.77	107.36
25619	193.88	2.98	98%	274.38	108.29
13353	101.42	6.77	99%	275.78	68.9
7225	610.95	103.39	98%	276.52	112.14
1175	89.72	12.52	98%	319.98	143.49
4314	199.22	16.19	98%	324.04	72.64
21281	119	14.89	99%	329.77	91.62
699	744.08	166.35	98%	385.87	84.98
17281	191.29	11.48	99%	407.86	108.78
7697	126.05	9.16	99%	418.46	147.54
24012	650.52	28.61	99%	423.59	476.52
5339	1561.45	746.53	98%	471.48	259.27
1561	1103.42	310.4	98%	483.63	109.78
24228	1037.63	336.37	98%	510.12	105.18
5616	1252.37	399.53	98%	617.19	131.84
15189	2393.48	562.64	98%	642.89	398.85
563	1286.12	293.65	98%	647.49	154.22
19392	1380.71	448.01	98%	669.42	123.39
21740	2258.4	588.09	98%	701.14	280.06
1854	2250.76	618.07	99%	730.54	265.59
3292	2871.21	931.15	99%	892.15	311.65
22598	2831.24	966.7	98%	1051.05	357.55
21661	2797.22	982.49	98%	1087.36	376.19
21660	4837.56	1684.22	98%	1692.71	582.02
17167	4555.27	1157.69	98%	2481.92	715.65

TABLE SN: F	arly Diclofenac			Documen	t Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	
10667	411.83	248.79	97%	13.74	165.12
17695	47.26	305.83	96%		60.09
3452	91.31	23.32	97%	29.73	28.67
21421	5.58	8.51	95%	31.49	16.56
6222	-12.72	9.64	95%	32.02	30.46
14996	180.85	117.09	98%	32.69	45.29
12844	-11.84	8.74	96%	39.54	27.67
1843	88.96	20.57	96%	48.67	17.77
9635	-9.83	19.06	95%	48.68	40.62
21707	169.82	64.58	95%	59.13	53.37
	37.52	28.79	96%	62.8	26.58
23302	l	79.49	95%	63.9	55.2
13932	-63.25 24.17	7.4	97%	65.08	25.49
18604		86.86	98%	66.15	50.9
20354	220.66		95%	69.83	46.13
1841	188.63	53.81	97%	71.24	34.86
355	149.37	52.24		77.75	25.92
17683	40.01	12.49	96%		44.73
2359	17.87	8.17	98%	86.55	
3713	168.44	419.14	97%	89.98	96.34
11840	51.82	10.03	96%	100.7	37.97
19211	88.71	85.04	96%	108.71	56.23
17800	70.19	39.86	98%	118.7	28.58
1844	277.5	69.37	96%	129.25	44.39
356	249.59	82.38	98%	129.82	46.84
23494	49.03	10.06	96%	131.42	50.45
14776	49.01	22.62	97%	134.61	47.31
23626	251.41	69.01	97%	141.32	90.59
23491	85.95	100.32	96%	155.17	56.53
21382	60.1	10.48	95%	162.86	70.74
6213	75.91	24.03	97%	177.43	53.8
15170	66.01	17.61	95%	180.78	58.76
23182	47.61	14.34	95%	182.97	82.24
14958	77.51	24.88	99%	192.52	57.74
16562	315.91	84.36	96%	194	49.14
23043	116.23	50.3	97%	200.45	58.35
18996	115.11	26.79	96%	211.48	69.45
14997	807.1	529.54	98%	231.67	129.71
10879	84.17	41	95%	235.09	83.29
11021	90.03	69.2	95%	247.67	106.37
2655	43.2	16.5	97%	258.1	178.54
16859	704.09	252.4	97%	258.84	124.37
17794	130.88	63.44	97%	261.13	86.21
6919	1235.49	468.87	99%	269.17	229.63
13353	151.45	114.9	97%	276.39	67.85

TABLE 2N: E	arly Dictofenac			Documen	t Number 1650775
	Group Mean	Group Stdev	LDA Score	Non Group Mean	
20	432.75	81.44	97%	277.59	75.26
12964	106.32	33.26	95%	288.44	95.46
3722	585.01	101.14	97%	295.66	101.48
20715	308.31	50.21	96%	313.11	180.79
23606	668.08	172.75	97%	313.49	105.76
23230	176.98	99.78	98%	342.52	164.69
12946	142.18	31.13	97%	349.51	100.28
24200	1265.26	395.08	97%	369.8	208.75
16768	264.62	55.65	95%	376.13	78.38
12857	231.61	293.1	96%	392.81	143.31
	726.51	149.33	97%	395.27	107.88
18795	654.92	135.45	97%	397.11	105.29
19		157.61	95%	402.03	119.63
18783	716.54	79.84	95%	410.59	104.1
19252	288.39	101.99	96%	427.86	137.39
1114	645.09	381.61	97%	479.92	178.44
20698	914.65	394.89	99%	521.35	157.69
21098	1119.71	345.03	98%	525.66	142.61
21097	883.9		99%	528.3	355.46
15191	1868.16	232.88	96%	529.59	254.13
19373	957.63	171.61		537.58	150.22
9424	1020	141.63	96%		142.5
15606	331.04	100.93	95%	555.14	466.99
4670	2609.57	936.24	97%	576.03	131.13
402	1115.89	448.86	99%	596.85	178.89
13557	267.85	27.9	96%	601.37	88.63
2368	429.73	38.72	96%	606.25	470.92
22906	2134.54	974.52	97%	617.58	391.8
15189	1986.69	445.74	98%	635.58	378.72
15190	2159.12	392.22	99%	661.42	244.32
1995	1259.5	439.49	98%	684.23	304.27
11830	1983.61	566.45	98%	692.89	
1805	1229.6	164.21	97%	703.35	218.45
1174	1340.59	440.4	96%	726.33	411.01
6013	1139.77	436.67	96%	749.39	184.56
17785	1846.83	672.05	97%	752.99	445.33
22840	1352.3	529.97	95%	755.78	273.45
8515	346.51	83	96%	765.99	292.49
21574	391.95	100	97%	817.75	226.02
6477	1367.6	542.86	97%	857.33	304.69
3292	1879.44	784.97	98%	890.76	323.1
12306	3293.83	1170.7	99%	1005.26	433.69
7451	1583.77	483.79	96%	1014.48	337.6
6295	2775.87	1040.34	99%	1068.45	493.12
21467	2391.61	1040.88	96%	1118.01	516.67

TABLE 3N:	Early Diclofena	Documer	nt Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
6633	2355.01	832.32	99%	1206.88	312.71
14738	2426.79	883.37	99%	1231.22	312.92
3730	2978.69	1180.6	98%	1232.87	586.1
3617	2869.63	1011.46	98%	1268.73	398.2
8715	3069.61	1101.03	99%	1353.63	759.44
17672	2889.9	351.84	96%	1930.21	397.38
26152	5392.56	2027.73	98%	1991.62	852.89
20846	4030.03	570.84	96%	2449.47	889.44
6018	11859.37	4320.03	98%	3477.55	3126.6

TABLE 30: Es	stradiol			Documer	nt Number 1650775
				Non Group Mean	Non Group Stdev
19476	221.25	108.8	94%	-58.59	73.88
20579		26.23	87%	-13.8	30.61
4520	74.3	35.09	90%	-1.56	34.15
55	34.69	14.89	86%	4.7	13.41
384	44.98	13.2	86%	5.76	28.49
22722	566.51	262.91	96%	19.66	47.88
12120	291.19	164.4	93%	20.32	48.27
16283	59.56	11.97	91%	25.04	15.43
10611	78.35	19.48	91%	26.01	28.58
3570	1203.99	486.89	96%	27.26	139.67
3929	66.1	15.81	88%	32.04	17.87
16783	94.16	35.66	86%	32.29	33.01
6604	9.87	7.84	88%	36.24	17.57
10540	70.62	15.26	85%	39.69	19.11
3846	63.36	11.22	85%	40.64	15.95
14266	463.56	161.4	95%	42	79.9
15097	-4.06	20.79	88%	44.39	28.23
16809	77.26	7.57	89%	53.84	28.46
672	185.2	45.2	92%	57.01	48.59
25290	322.26	83.7	94%	68.08	67.25
5493	104.13	22.09	86%	69.51	45.42
17699	379.25	121.82	95%	77.01	64.08
15057	178.76	62.35	89%	80.64	61.88
4082	137.71	29.22	87%	81.24	39.54
3074	305.3	91.43	94%	82.44	74.5
12655	222.74	65.14	88%	90.1	61.41
3073	404.03	113.1	94%	97.56	106.47
23220	158.44	34.05	86%	104.71	23.6
18612	214.55	48.01	88%	114.72	54.02
24442	253.1	51.52	95%	119.28	39.27
19258	345.84	102.07	91%	119.63	94.13
6789	266.72	63.61	88%	130.61	57.1
11465	687.63	230.97	94%	136.61	114.55
23491	259.04	44.02	89%	151.54	55.44
3075	515.63	145.3	94%	159.61	267.05
19261	291.37	82.45	86%	163.74	57.85
17393	223.13	34.27	86%	164.98	67.02
23987	254.16	41.43	86%	168.68	53.84
13229	314.84	68.95	90%	184.84	61.96
15295	252.4	28.26	85%	191.1	52.8
23183	91.05	26.84	85%	192.16	88.8
6549	522.38	151.13	89%	204.39	114.46
13092	440.75	124.27	92%	206.68	86.61
9402	278.52	27.55	85%	207.63	69.5

TABLE 30; Es	stradiol			Documer	nt Number 1650775
		Group Stdey	LDA Score	Non Group Mean	Non Group Stdev
23362	362.98	58.85	92%	209.03	55.26
729	141.14	32.05	85%	209.19	55.66
13963	572.36	193.21	91%	220.12	112.51
17516	287.34	30.47	85%	223.48	56.14
7927	368.05	56.64	86%	226.41	79.19
14989	306.39	34.48	90%	229.8	59.41
5464	608.63	139.88	93%	235.86	136.35
14997	313.77	45.38	92%	237.05	156.21
23337	388.86	61.57	87%	239.19	87.95
6541	835.22	410.07	90%	240.86	107.93
9621	349.89	41.41	91%	242.89	62.26
18877	1770.96	536.63	95%	251.02	323.54
19825	76.2	82.83	85%	256.34	107.9
291	413.96	84.34	85%	256.37	66.6
17613	349.67	47.08	86%	259.18	106.99
19824	83.21	81.92	87%	260.01	99.57
7684	577.91	188.77	85%	279.08	126.11
2373	634.92	150.17	92%	285.8	133.51
2484	57.67	44.88	86%	289.53	213.13
16684	447.2	65.17	88%	306.67	87.7
6975	700.83	228.78	86%	312.49	161.5
18141	1086.32	372.55	88%	330.82	216.89
25718	464.33	56.04	91%	331.59	76.26
18742	172.88	37.74	87%	352.25	190.08
12361	1014.46	256.68	94%	354.09	232.49
16327	558.02	61.36	88%	369.06	94.06
21164	169.42	47.37	86%	370.17	185.53
24012	2053.62	525.68	94%	382.21	392.09
4674	167.98	66.36	88%	452.2	224.88
6060	310.86	53.86	86%	477.05	121.08
1561	310.14	86.6	90%	491.78	117.97
11227	841.6	140.02	86%	496.07	212.99
19728	229.27	93.53	88%	501.97	174.65
12746	759.81	83.64	93%	520.3	104.48
12585	909.57	150.85	86%	542.79	178.84
23437	271.75	62.16	86%	558.17	246.21
11821	1051.26	228.29	86%	574.09	309.97
24707	407.68	85.92	85%	598.16	183.22
16894	1105.64	177.51	91%	731.2	332.55
11720	397.65	148.44	88%	748.93	265
4440	398.17	156.94	89%	804.73	210.24
7584	2336.91	636.07	91%	819.41	712.46
13093	2287.36	766.73	90%	825.52	505.38
11644	485.11	142.46	86%	838.95	238.55

TABLE 30: Estradiol Document Number 1650775							
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev		
9475	422.84	219.9	86%	958.81	372.8		
24112	1879.78	259.59	90%	1026.22	630.45		
16703	714.02	96.32	86%	1057.6	331.01		
15534	1418.23	154.26	88%	1104.88	261.78		
14738	862.34	156.54	85%	1256.55	349.62		
14960	1831.5	294.22	85%	1370.37	509.8		
22554	609.46	270.71	86%	1371.14	511.54		
6015	707.01	273.93	89%	1539.98	455.17		
7497	1136.4	136.44	87%	1691.66	329.88		

TARLE 3P1 L	ate Indomethaci	n		Docume	nt Number 1650775
GLGC ID	Group Mean		LDA Score	Non Group Mean	Non Group Stdev
21075	56.56	18.08	99%	-101.64	72.06
3626	270.02	126.67	99%	-91.68	41.85
20522	88.79	62.74	99%	-86.26	44.12
18203	28.03	7.89	100%	-59.65	26.67
21682	139.83	65.11	99%	-56.8	31.49
20119	75.13	51.9	99%	-51.89	22.95
945	164.01	44.63	98%	-32.43	36.01
8017	40.5	7.12	99%	-4.91	18.36
22516	427.71	48.74	100%	-3.53	27.61
7858	133.46	131.64	99%	-2.18	10.32
11731	57.13	15.61	99%	-1.13	13.51
2011	88.53	22.86	99%	5.7	10.46
19121	104.23	50.09	99%	16.77	12.76
24826	218.27	46.71	99%	17.2	179.73
23555	133.19	49.37	99%	22.23	20.8
21445	313.48	71.78	99%	22.36	29.24
1777	117.77	21.2	99%	22.67	16.4
16173	249.12	60.67	99%	23.05	21.76
21683	179.43	48.48	99%	24.37	26.58
19503	106.66	42.52	99%	24.54	12.74
19444	479	225.49	99%	26.17	29.3
20651	252.93	78.27	99%	26.84	24.52
11172	108.09	14.64	99%	27.38	25.08
7196	70.2	6.99	99%	27.5	18.37
8864	168.51	38.98	98%	28.16	40.98
25052	413.35	149.76	98%	28.65	72.19
12277	188.8	30.97	99%	28.87	27.27
20134	115.79	25.97	99%	31.07	21.72
15961	155.48	44.33	99%	31.59	27.65
22897	135.13	41.74	99%	33.43	19.08
1893	250.46	53.73	99%	40.37	21.42
22512	493.75	186.61	99%	40.54	35.84
14081	1307.16	578.37	99%	40.73	109.27
25083	96.77	17.16	99%	41.1	19.54
17500	182.9	29.18	100%	43.12	42.04
2013	191.84	31.9	99%	44.55	23.34
8273	410.92	194.88	99%	45.89	30.96
19411	184.69	32.53	99%	46.1	23.55
15504	896.04	321.22	99%	46.28	53.42
22514	543.21	150.84	99%	57.67	44.72
155	187.91	27.8	99%	62.07	21.49
20523	337.44	89.8	98%	66.71	58.22
16961	225.29	41.42	99%	71.58	40.53
24589	412.43	149.59	98%	73.14	30.15

TABLE 3P: L	ate Indomethaci	n		Docume	nt Number 1650775
	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21285	903.94	338.62	99%	73.28	108.74
15503	519.54	109.49	100%	74.61	27.28
6200	1572.18	522.18	99%	78	145.78
7743	288.96	85.4	98%	83.77	52.71
2012	357.34	70.02	99%	84.87	34.39
3749	-48.1	12.54	99%	87.36	48.17
4892	2121.77	1018.81	99%	97.96	339.86
24651	168.51	30.23	98%	98.36	20.05
23005	536.62	86.56	99%	99.43	90.49
1700	273.11	39.16	99%	102.11	30.56
22898	507.42	174.82	99%	103.97	57.4
8522	552.47	146.35	99%	105.43	54.02
12714	0.7	18.22	98%	106.47	34.92
15116	243.85	52.64	98%	107.4	25.94
17277	239.1	35.46	99%	107.78	39.78
22042	21.05	10.38	98%	109.25	91.56
21414	1412.18	189.99	99%	116.04	143.33
17258	235.7	32.66	99%	120.39	25.05
682	555.72	137.48	99%	126.28	58.1
17369	441.37	64.2	99%	130.38	54.83
20529	790.13	186.87	99%	134.07	101.45
14504	773.65	116.14	99%	147.38	84.22
154	347.17	63.6	99%	154.37	37.49
12450	-60.33	24.42	99%	154.48	84.94
6431	1828.3	421.64	99%	190.99	149.33
18580	1167.73	411.76	99%	193.7	141.11
8310	107.35	13.86	99%	204.96	44.79
14330	633.28	126.05	99%	225.12	77.1
5687	48.78	22.59	99%	227.66	79.73
14185	760.34	170.85	99%	253.08	93.43
21443	569.4	110.65	99%	256.7	61.78
16519	807.19	191.58	98%	273.02	117.31
9079	820.52	184.52	98%	316.54	112.19
19469	162.04	26.75	99%	325.82	57.22
373	115.43	31.34	99%	334.03	85.91
43	156.53	22.34	99%	341.11	74.71
20864	37.65	12.15	100%	352.3	179.09
699	762.57	112.9	99%	383.6	79.72
24323	230.34	24.71	99%	398.78	95.09
17281	100.34	30.42	99%	410.15	105.21
16366	113.72	34.12	99%	439.22	103.99
21014	188.22	42.97	99%	572.37	137.02
16367	166.59	86.34	99%	612.27	144.06
25525	264.07	72.58	99%	645.12	117.62

TABLE 3P:	Late Indometha	cin	Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
635	308.38	68.87	99%	672.17	126.74
18890	126.36	42.96	99%	679.93	361.87
634	355.69	72.95	99%	705.77	125.16
6236	227.28	73.91	98%	902.24	429.28
10984	135.85	78.66	99%	1092.48	362.92
15029	181.72	50.19	99%	1492.95	529.6
4933	357.28	114.44	99%	1702.56	598.89

TABLE 3Q: E	arly Indomethad	cin		Documer	nt Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21682	85.12	87.03	93%	-56.37	33.66
1510	75.53	7.54	96%	-13.1	65.66
26280	109.21	31.74	89%	-10.05	85.78
11422	60.74	22.85	91%	13.75	11.38
1507	46.96	9.51	87%	15.4	15.74
16251	34.42	5.87	90%	20.02	13.62
19671	39.81	7.46	90%	22.33	14.64
23106	48.6	11.99	93%	28.28	33.85
2736	49.82	5.14	93%	29.89	18.47
25077	111.99	30.35	88%	30.69	73.6
1221	445.47	178.19	92%	33.57	94.3
18389	94.31	16.02	94%	33.62	32.95
3972	-24.58	15.09	94%	34.18	35.89
18237	63.23	7.16	91%	36.35	20.91
22725	4.84	8.57	88%	36.54	24.3
17854	94.21	22.12	90%	48.6	21.13
25379	64.97	7.1	91%	48.71	16.47
1843	85.73	19.01	94%	48.71	17.88
4504	96.84	28.13	90%	48.77	77.49
24024	75.74	15.08	90%	50.05	33.85
16809	117.87	32.17	90%	53.62	27.39
11423	102.73	23.05	89%	54.5	20.13
2042	92.88	5.97	96%	54.98	50.98
13992	110.02	45.53	90%	55.81	24.86
22918	27.24	5.2	92%	57.51	29.32
5059	222.71	98.2	92%	61.9	61.99
20354	194.32	79.46	91%	66.49	51.97
18529	139.38	36.52	88%	68.68	53.21
8079	-1.13	28.24	91%	70.82	43.57
7176	83.8	6.04	89%	71.68	21.23
24721	116.01	17.12	91%	75.35	29.71
11904	169.62	30.75	91%	81.73	37.23
3710	-40.52	24.79	89%	84.89	112.56
1271	127.09	19.36	88%	87.87	22.54
15207	207.84	67.65	90%	88.03	53.57
21256	150.53	29.3	87%	90.66	43.12
1572	134.45	17.05	87%	92.3	26.58
19410	154.21	25.11	89%	95.44	23.68
16080	172.16	50.03	89%	95.77	117.15
17950	134.99	16.51	87%	96.23	39.64
22321	169.07	47.34	95%	101.03	89.08
9223	166.07	27.83	88%	106.75	43.32
17277	186.86	45.28	88%	108.27	41.12
16125	212.34	60.78	90%	109.55	34.54

TABLE 30: E	arly Indomethac	in .		Documer	it Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
354	156.92	39.75	88%	113.78	121.78
22151	49.94	21.66	90%	114.35	59.07
16477	205.91	47.02	87%	118.16	42.37
15884	197.78	19.66	96%	119.51	58.67
25768	189	17.68	94%	128.02	30.12
6532	275.04	58.08	92%	135.65	42.31
2555	342.38	116.88	91%	141.73	57.69
25370	95.55	12.34	87%	141.81	76.1
1426	186.05	11.71	91%	141.89	28.02
16081	293.29	79.31	90%	147.43	146.68
154	240.39	32.25	90%	155.47	42.04
1521	271.17	53.27	87%	157.16	61.75
22806	82.54	19.97	89%	169.69	77.1
1141	221.49	23.61	89%	172.77	35.13
9595	369.54	72.63	90%	176.26	67.68
21709	240.64	11.92	95%	179.9	33.86
13332	111.82	16.97	88%	187.21	61.88
	292.61	40.73	91%	204.56	58.9
21444		45.66	91%	216.95	69.67
20350	333.21	58.6	88%	226.04	54.29
3776	316.54	16	89%	240.09	72.64
958	283.88	40.8	91%	245.89	190.12
18891	63.95	48.25	89%	247.11	88.8
15786	130.41	128.09	87%	254.11	122.09
22619	509.69		90%	257.67	178.99
2655	76.89	36.89	90%	258.32	68.58
21443	408.93	75.59	90%	309.86	189.82
17664	718.76	159.35	87%	340.51	149.15
1795	179.95	54.13	89%	342.19	121.17
6825	188.01	57.66 68.3	93%	353.78	236.17
18465	583.12	156.59	91%	364.41	124.75
19412	798.48	324.83	92%	368.96	133.71
4026	854.17	51.68	88%	381.94	139.96
20915	208.25	114.76	89%	391.56	105.49
12463	631.37		89%	421.1	129.61
7122	778.65	154.65		453.5	126.98
23245	695.04	100.61	88%	496.14	169.1
20701	818.5	138.91	88%	520.99	516.04
23125	203.3	56.02 289.81	91%	701.6	296.47
21740	1357.78	80.79	89%	722.78	196.14
16458	933.78	333.85	92%	731.5	257.06
11720	1393.76		89%	922.94	660.67
23449	166.05	104.49	87%	1063.27	404.32
23989	1702.06	285.92			343.44
22368	637.02	202.48	88%	1081.65	1040.44

TABLE 3Q: Early Indomethacin Document Number 1650775					
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
24289	672.7	120.08	88%	1097.27	342.03
16885	837.41	195.77	91%	1485.4	407.68
9267	809.11	323.93	92%	1667.39	543.29

TABLE 3R: \	/alproate			Docume	nt Number 1650775
	Group Mean	Group Stdev			Non Group Stdev
26190	239.04	44.21	99%	-115.53	71.46
2154	26.52	22.45	98%	-34	15.98
12625	129.76	35.25	98%	-7.97	79.74
4231	160.07	13.84	100%	-6.47	34.51
360	42.77	15.77	97%	-5.58	16.63
24126	127.21	24.22	97%	6.68	31.59
8993	64.31	7.77	99%	8.92	10.71
19762	168.43	71.93	99%	9.69	24.52
11336	60.09	15.29	99%	12.42	10.72
20993	73.86	17.79	98%	12.51	23.49
330	76.9	11.84	98%	13.5	26.03
12058	48.89	5.96	98%	16.85	15.53
1579	75.5	19.78	98%	16.86	13.09
5993	49.43	5.91	97%	17.56	13.02
8054	63.83	11.7	97%	17.56	15.18
23315	53.08	6.14	98%	20.16	11.05
23843	102.85	21.92	99%	21.2	18.22
11315	170.88	30.14	98%	22.9	42.27
13812	138.26	33.46	99%	26.62	22.64
23106	97.66	12.04	99%	28.05	33.33
	70.95	9.83	97%	28.43	16.22
11625	155.52	11.78	99%	30.44	41.52
9374	+	57.19	99%	35.12	29.91
10394	210.39	49.53	97%	38.17	25.87
6101 2117	146.33	17.82	97%	43.75	19.24
	113.54	14.75	98%	45.51	37.01
12614	130.53	51.66	98%	47.22	33.17
9766 2932	256.87	86.84	98%	48.26	30.66
13501	145.64	35.69	98%	48.87	22.87
	145.04	21.59	98%	51.42	27.75
14913	133.08	23.07	98%	53.6	21.07
16673		50.07	98%	54.55	49.7
2042	183.57 150.2	35.95	98%	55.29	23.13
2915	· · · · · · · · · · · · · · · · · · ·	28.28	99%	60.25	31.79
19669 19264	192.83	13.12	98%	62.26	25.95
17257	197.58	17.21	99%	67.22	34.6
	157.22	12.55	98%	67.92	42.04
15663	186.56	12.56	97%	68.89	53.83
11527	201.22	32.17	99%	75.66	28.1
22375	289.15	110.18	98%	82.52	54.48
5754		5.38	99%	83.53	37.27
12198 18885	157.09 179.92	14.06	99%	85.54	27.13
13166	392.55	98.9	98%	89.27	56.47
		11.85	97%	89.73	88.96
13251	155.07	[11.00	131 /0	100.70	100.00

TABLE 3R: V	/alnroate			Docume	nt Number 1650775
GLGC ID	Group Mean	Group Stdev		Non Group Mean	
8728	346.01	114.17	98%	90.12	40.25
2216	234.47	28.59	99%	94.87	37.16
21535	197.23	12.53	98%	96.15	38.42
21567	509.19	66.46	98%	97.9	104.57
10593	328.02	63.73	99%	101.91	43.97
17368	241.72	37.58	97%	104.44	49.02
9800	366.46	11.6	99%	105.66	68.67
17479	261.87	40.08	99%	106.14	33.44
21976	256.5	24.3	98%	106.4	45.51
14600	242.39	40.76	98%	111.36	76.44
	241.74	26.13	97%	111.56	44.08
22570 23656	273.7	31.03	98%	112.56	52.23
	255.98	37.97	98%	112.9	41.1
15179	304.19	58.02	98%	115.37	49.86
16616 5608	233.3	11.25	97%	122.33	53.28
	263.76	45.31	98%	126.59	32.66
20090		52.99	98%	128.35	68.07
17644	333.21	64.29	97%	128.59	59.92
15149	345.13	53.49	99%	133.02	59.87
6789	283.91	41.65	99%	139.06	46.36
6686	369.2		98%	149.61	84.83
19230	391.37	57.35 6.84	99%	151.24	58.29
13949	47.22	36.75	98%	159.37	38.65
11280	287.5	59.75	97%	163.49	60.93
19513	345.16	26.82	97%	164.97	66.22
23762	321.28	30.14	99%	166.7	55.87
13838	437.29	12.09	98%	168.14	70.13
2691	316.24	66.85	99%	168.33	60.29
9572	409.53 397.87	34.78	100%	168.71	47.4
6861	361.16	95.89	98%	170.63	47.21
22135	283.3	44.23	98%	172.33	155.38
24388	403.05	74.14	98%	175.49	63.14
18886	602.67	63.22	99%	183.22	79.82
24368 5381	356.13	13.85	99%	191.57	49.01
9402	342.47	21.74	97%	208.49	68.96
17261	546.81	71.98	99%	219.95	72.35
	430.5	35.07	99%	224.81	67.09
2101	546.78	56.44	97%	228.98	103.39
24369 11354	530	66.53	99%	229.49	68.24
8709	90.79	24.72	98%	233.09	61.98
24367	400.74	12.79	99%	245.59	55.58
19052	646.73	83.13	98%	254.53	92.68
22957	665.35	87.82	98%	274.44	208.86
15551	493.87	26.61	99%	304.36	63.07

TABLE 3R: Valproate			- 4	Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev	
12317	639.88	73.89	99%	308.65	88.02	
4179	845.91	78.29	98%	333.97	135.14	
6440	961.78	166.32	97%	351.53	186.44	
7111	553.56	43.59	98%	353.19	75.73	
18285	707.67	76.76	99%	357.46	132.75	
12928	791.23	86.89	98%	410.91	94.08	
15051	1110.61	136.73	97%	476.75	412.42	
2569	338.95	14.84	98%	721.15	290.78	
3803	499.92	74.41	97%	920.04	208.7	
18962	573.38	98.13	99%	1606.33	624.84	
5052	906.23	65.55	99%	1930.67	442.76	
22540	1108.89	178.44	97%	2311.11	657.83	

TABLE 3S:	MV-14643			Documer	nt Number 1650775
	Group Mean	Group Stdev	LDA Score	Non Group Mean	
3175	81.67	38.5	98%	-24.57	20
2051	31.61	16.91	98%	-19.67	25.77
23627	40.97	4.93	98%	-14.82	37.36
16409	95.86	23.34	97%	-8.25	35.38
14116	38.83	17.55	99%	-7.83	5.25
18029	208.84	94.33	98%	-7.23	21.53
6677	32.1	15.65	98%	-6.62	9.95
20856	275.88	94.5	99%	-5.26	14.41
5565	221.64	85.1	97%	17.46	47.37
12467	216.39	65.04	99%	20.32	20.78
	148.59	59.24	99%	22.05	17.54
23500	529	114.56	99%	23.94	68.23
1858		9.86	99%	28.61	31.53
8820	81.06	31.47	99%	29.7	16.97
18082	128.62		97%	33.8	32.95
4931	135.4	29.63	98%	42.43	17
9925	117.26	29.18			17.97
24381	97.68	12.7	98%	43.65 43.76	16.97
6292	96.5	10.27	98%		14.44
5518	-34.55	15.68	100%	44.56	
18083	370.91	74.26	98%	45.23	60.06
4272	590.58	82.76	100%	47.77	61.51
7295	114.22	11.36	98%	48.54	27.07
8315	251.82	52.39	98%	50.52	44.35
20855	205.89	56.89	100%	51.41	13.97
15018	153.93	12.99	97%	51.69	40.82
22046	173.79	36.81	97%	52.05	35.05
4438	-53.05	31.71	99%	53.83	12.81
18956	233.24	49.47	99%	57.47	28.38
3631	135.16	24.43	97%	62.18	23.06
4271	1146.85	102.6	100%	63.33	94.28
6553	215.81	43.91	97%	64.81	42.7
3558	192.81	32.74	98%	65.12	31.67
20038	306.38	66.25	98%	68.41	50.76
7517	190.58	26.66	98%	71.67	32.59
3743	185.35	31.74	99%	71.95	25.24
14507	291.71	54.52	98%	74.57	66.85
18749	288.03	90.54	98%	77.94	40.13
4290	293.68	45.21	98%	87.32	46.32
14595	321.16	55.3	98%	89.33	56.57
14264	331.35	82.51	98%	91.8	58.3
397	232.66	39.79	99%	91.99	32.22
18746	280.52	43.35	98%	93.45	48.78
3439	244.57	26.7	99%	100.37	28.67
2190	164.79	17.03	97%	100.78	189.02

TABLE 3S:	WY-14643			Documer	nt Number 1650775
GLGC ID	Group Mean		LDA Score	Non Group Mean	Non Group Stdev
18318	279.93	40.82	98%	111.57	48.48
5887	1076.32	275.73	99%	111.64	138.98
3513	212.58	33.36	98%	114.18	27.84
22416	1001.99	170.33	99%	121.52	83.97
22224	487.47	76.85	99%	124.54	72.09
12215	632.99	209.38	98%	141.79	100.45
9373	419.3	49.02	98%	144.86	76.23
15672	378.23	65.03	98%	151.17	68.05
3260	508.28	175.97	98%	153.29	72.65
16700	596.39	103.44	99%	155.05	96.4
18747	457.04	82.08	97%	155.98	76.29
26109	1286.05	121.59	99%	156.58	201.4
22737	685.5	206.71	99%	168.28	96.83
3720	315.08	30.72	98%	179.69	49.62
2113	410.43	34.36	99%	185.32	58.03
15015	374.26	31.51	99%	192.11	63.36
6439	425.56	74.96	97%	196.56	74.01
22370	945.85	62.98	100%	216.15	108.38
2457	1132.75	158.6	99%	227.31	140.2
1728	477.23	66.78	98%	227.92	60.65
18891	1245.42	225.38	99%	230.61	151.12
22620	386.56	21.42	98%	235.22	68.77
19591	567.11	40.94	99%	237.04	108.52
5602	1404.36	215.76	99%	242.82	212.8
24860	67.15	34.2	97%	279.45	115.83
22392	598.76	55.66	99%	296.04	67.51
18742	1303.27	263.5	99%	335.32	154.05
6825	626.39	47.06	98%	336.52	118
21164	991.37	155.11	99%	356.95	172.12
9372	1244.96	107.3	99%	368.29	225.64
8177	121.78	23.64	97%	389.45	423.88
17935	1404.15	220.52	97%	416.54	273.3
10533	1054.36	147.32	98%	421.36	212.4
16944	747.42	72.2	98%	422.41	133.98
21354	2186.83	317.02	98%	437.51	348.77
16323	223.57	44.79	99%	465.4	220.36
9423	273.32	30.42	98%	486.76	134.12
19044	814.58	45.86	97%	502.31	184.58
18727	206.23	25.52	99%	516.82	179.53
18125	1062.51	80.83	99%	529.14	174.32
16704	1486.63	221.63	97%	565.52	242.61
3099	922.46	83.44	97%	599.33	119.33
2813	1250.39	172.69	98%	603.02	185.25
20998	325.2	72.5	97%	606.04	134.27

TABLE 3S: WY-14643				Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev	
21010	1699.76	218.74	98%	606.25	249.41	
14882	377.63	34.39	97%	607.89	168.14	
5616	386.99	47.15	97%	623.82	140.57	
16945	1098.96	98.19	98%	628.67	192.67	
7420	1415.94	79.85	97%	655.69	311.93	
18890	1900.82	258.12	99%	657.78	337.82	
3279	1571.19	374.24	98%	708.13	199.08	
16190	1581.05	206.33	98%	716.2	226.42	
20597	378.94	48.6	98%	742.21	189.37	
21341	1797.23	203.99	98%	768.53	328.94	
4940	623.22	140.4	98%	1632.44	469.8	

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